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(54) Title: ENVIRONMENTAL STRESS TOLERANCE GENES

(57) Abstract: Recombinant polynucleotides and methods for modifying the phenotype of a plant are provided. In particular, the phenotype that is being modified is a plant's environmental stress tolerance.

WO 01/36598 A1



ENVIRONMENTAL STRESS TOLERANCE GENES

RELATED APPLICATION INFORMATION

5 The present invention claims the benefit from US Provisional Patent Application Serial Nos. 60/166,228 filed November 17, 1999 and 60/197,899 filed April 17, 2000 and "Plant Trait Modification III" filed August 22, 2000.

FIELD OF THE INVENTION

This invention relates to the field of plant biology. More particularly, the present invention pertains to compositions and methods for phenotypically modifying a plant.

10 **BACKGROUND OF THE INVENTION**

Transcription factors can modulate gene expression, either increasing or decreasing (inducing or repressing) the rate of transcription. This modulation results in differential levels of gene expression at various developmental stages, in different tissues and cell types, and in response to different exogenous (e.g., environmental) and endogenous stimuli
15 throughout the life cycle of the organism.

Because transcription factors are key controlling elements of biological pathways, altering the expression levels of one or more transcription factors can change entire biological pathways in an organism. For example, manipulation of the levels of selected transcription factors may result in increased expression of economically useful proteins or
20 metabolic chemicals in plants or to improve other agriculturally relevant characteristics. Conversely, blocked or reduced expression of a transcription factor may reduce biosynthesis of unwanted compounds or remove an undesirable trait. Therefore, manipulating transcription factor levels in a plant offers tremendous potential in agricultural biotechnology for modifying a plant's traits.

25 The present invention provides novel transcription factors useful for modifying a plant's phenotype in desirable ways, such as modifying a plant's environmental stress tolerance.

SUMMARY OF THE INVENTION

In a first aspect, the invention relates to a recombinant polynucleotide comprising a nucleotide sequence selected from the group consisting of: (a) a nucleotide sequence encoding a
30 polypeptide comprising a sequence selected from SEQ ID Nos. 2N, where N=1-27, or a complementary nucleotide sequence thereof; (b) a nucleotide sequence encoding a polypeptide comprising a conservatively substituted variant of a polypeptide of (a); (c) a nucleotide sequence comprising a sequence selected from those of SEQ ID Nos. 2N-1, where N=1-27, or a

complementary nucleotide sequence thereof; (d) a nucleotide sequence comprising silent substitutions in a nucleotide sequence of (c); (e) a nucleotide sequence which hybridizes under stringent conditions over substantially the entire length of a nucleotide sequence of one or more of: (a), (b), (c), or (d); (f) a nucleotide sequence comprising at least 15 consecutive nucleotides of a sequence of any of (a)-(e); (g) a nucleotide sequence comprising a subsequence or fragment of any of (a)-(f), which subsequence or fragment encodes a polypeptide having a biological activity that modifies a plant's environmental stress tolerance; (h) a nucleotide sequence having at least 30% sequence identity to a nucleotide sequence of any of (a)-(g); (i) a nucleotide sequence having at least 60% identity sequence identity to a nucleotide sequence of any of (a)-(g); (j) a nucleotide sequence which encodes a polypeptide having at least 30% identity sequence identity to a polypeptide of SEQ ID Nos. 2N, where N=1-27; (k) a nucleotide sequence which encodes a polypeptide having at least 60% identity sequence identity to a polypeptide of SEQ ID Nos. 2N, where N=1-27; and (l) a nucleotide sequence which encodes a conserved domain of a polypeptide having at least 65% sequence identity to a conserved domain of a polypeptide of SEQ ID Nos. 2N, where N=1-27. The recombinant polynucleotide may further comprise a constitutive, inducible, or tissue-active promoter operably linked to the nucleotide sequence. The invention also relates to compositions comprising at least two of the above described polynucleotides.

In a second aspect, the invention is an isolated or recombinant polypeptide comprising a subsequence of at least about 15 contiguous amino acids encoded by the recombinant or isolated polynucleotide described above.

In another aspect, the invention is a transgenic plant comprising one or more of the above described recombinant polynucleotides. In yet another aspect, the invention is a plant with altered expression levels of a polynucleotide described above or a plant with altered expression or activity levels of an above described polypeptide. Further, the invention may be a plant lacking a nucleotide sequence encoding a polypeptide comprising a sequence selected from SEQ ID Nos. 2N, where N=1-27.

The plant may be a soybean, wheat, corn, potato, cotton, rice, oilseed rape, sunflower, alfalfa, sugarcane, turf, banana, blackberry, blueberry, strawberry, raspberry, cantaloupe, carrot, cauliflower, coffee, cucumber, eggplant, grapes, honeydew, lettuce, mango, melon, onion, papaya, peas, peppers, pineapple, spinach, squash, sweet corn, tobacco, tomato, watermelon, rosaceous fruits, or vegetable brassicas plant.

In a further aspect, the invention relates to a cloning or expression vector comprising the isolated or recombinant polynucleotide described above or cells comprising the cloning or expression vector.

In yet a further aspect, the invention relates to a composition produced by incubating a polynucleotide of the invention with a nuclease, a restriction enzyme, a polymerase; a polymerase and a primer; a cloning vector, or with a cell.

Furthermore, the invention relates to a method for producing a plant having
5 improved environmental stress tolerance. The method comprises altering the expression of an isolated or recombinant polynucleotide of the invention or altering the expression or activity of a polypeptide of the invention in a plant to produce a modified plant, and selecting the modified plant for modified environmental stress tolerance.

In another aspect, the invention relates to a method of identifying a factor that is
10 modulated by or interacts with a polypeptide encoded by a polynucleotide of the invention. The method comprises expressing a polypeptide encoded by the polynucleotide in a plant; and identifying at least one factor that is modulated by or interacts with the polypeptide. In one embodiment the method for identifying modulating or interacting factors is by detecting binding by the polypeptide to a promoter sequence, or by detecting interactions between an additional
15 protein and the polypeptide in a yeast two hybrid system, or by detecting expression of a factor by hybridization to a microarray, subtractive hybridization or differential display.

In yet another aspect, the invention is a method of identifying a molecule that modulates activity or expression of a polynucleotide or polypeptide of interest. The method comprises placing the molecule in contact with a plant comprising the polynucleotide or
20 polypeptide encoded by the polynucleotide of the invention and monitoring one or more of the expression level of the polynucleotide in the plant, the expression level of the polypeptide in the plant, and modulation of an activity of the polypeptide in the plant.

In yet another aspect, the invention relates to an integrated system, computer or computer readable medium comprising one or more character strings corresponding to a
25 polynucleotide of the invention, or to a polypeptide encoded by the polynucleotide. The integrated system, computer or computer readable medium may comprise a link between one or more sequence strings to a modified plant environmental stress tolerance phenotype.

In yet another aspect, the invention is a method for identifying a sequence similar or homologous to one or more polynucleotides of the invention, or one or more polypeptides
30 encoded by the polynucleotides. The method comprises providing a sequence database; and, querying the sequence database with one or more target sequences corresponding to the one or more polynucleotides or to the one or more polypeptides to identify one or more sequence members of the database that display sequence similarity or homology to one or more of the one or more target sequences.

The method may further comprise of linking the one or more of the polynucleotides of the invention, or encoded polypeptides, to a modified plant environmental stress tolerance phenotype.

BRIEF DESCRIPTION OF THE DRAWINGS

Figure 1 provides a table of exemplary polynucleotide and polypeptide sequences of the invention. The table includes from left to right for each sequence: the SEQ ID No., the internal code reference number (GID), whether the sequence is a polynucleotide or polypeptide sequence, and identification of any conserved domains for the polypeptide sequences.

Figure 2 provides a table of exemplary sequences that are homologous to other sequences provided in the Sequence Listing and that are derived from *Arabidopsis thaliana*. The table includes from left to right: the SEQ ID No., the internal code reference number (GID), identification of the homologous sequence, whether the sequence is a polynucleotide or polypeptide sequence, and identification of any conserved domains for the polypeptide sequences.

Figure 3 provides a table of exemplary sequences that are homologous to the sequences provided in Figures 1 and 2 and that are derived from plants other than *Arabidopsis thaliana*. The table includes from left to right: the SEQ ID No., the internal code reference number (GID), the unique GenBank sequence ID No. (NID), the probability that the comparison was generated by chance (P-value), and the species from which the homologous gene was identified.

DETAILED DESCRIPTION

The present invention relates to polynucleotides and polypeptides, e.g. for modifying phenotypes of plants.

In particular, the polynucleotides or polypeptides are useful for modifying traits associated with a plant's environmental stress tolerance when the expression levels of the polynucleotides or expression levels or activity levels of the polypeptides are altered. Specifically, the polynucleotides and polypeptides are useful for modifying traits associated with a plant's environmental stress tolerance, such as freezing, chilling, heat, drought, water saturation, salt, photoconditions, radiation and ozone, or the like. Plants with altered expression of the polynucleotides or polypeptides of the invention are more tolerant to these environmental stresses compared with plants without altered expression levels.

The polynucleotides of the invention encode plant transcription factors. The plant transcription factors are derived, e.g., from *Arabidopsis thaliana* and can belong, e.g., to one

or more of the following transcription factor families: the AP2 (APETALA2) domain transcription factor family (Riechmann and Meyerowitz (1998) J. Biol. Chem. 379:633-646); the MYB transcription factor family (Martin and Paz-Ares (1997) Trends Genet. 13:67-73); the MADS domain transcription factor family (Riechmann and Meyerowitz (1997) J. Biol. Chem. 378:1079-1101); the WRKY protein family (Ishiguro and Nakamura (1994) Mol. Gen. Genet. 244:563-571); the ankyrin-repeat protein family (Zhang et al. (1992) Plant Cell 4:1575-1588); the miscellaneous protein (MISC) family (Kim et al. (1997) Plant J. 11:1237-1251); the zinc finger protein (Z) family (Klug and Schwabe (1995) FASEB J. 9: 597-604); the homeobox (HB) protein family (Duboule (1994) Guidebook to the Homeobox Genes, Oxford University Press); the CAAT-element binding proteins (Forsburg and Guarente (1989) Genes Dev. 3:1166-1178); the squamosa promoter binding proteins (SPB) (Klein et al. (1996) Mol. Gen. Genet. 196 250:7-16); the NAM protein family; the IAA/AUX proteins (Rouse et al. (1998) Science 279:1371-1373); the HLH/MYC protein family (Littlewood et al. (1994) Prot. Profile 1:639-709); the DNA-binding protein (DBP) family (Tucker et al. (1994) EMBO J. 13:2994-3002); the bZIP family of transcription factors (Foster et al. (1994) FASEB J. 8:192-200); the BPF-1 protein (Box P-binding factor) family (da Costa e Silva et al. (1993) Plant J. 4:125-135); and the golden protein (GLD) family (Hall et al. (1998) Plant Cell 10:925-936).

In addition to methods for modifying a plant phenotype by employing one or more polynucleotides and polypeptides of the invention described herein, the polynucleotides and polypeptides of the invention have a variety of additional uses. These uses include their use in the recombinant production (i.e., expression) of proteins; as regulators of plant gene expression, as diagnostic probes for the presence of complementary or partially complementary nucleic acids (including for detection of natural coding nucleic acids); as substrates for further reactions, e.g., mutation reactions, PCR reactions, or the like, or as substrates for cloning e.g., including digestion or ligation reactions, and for identifying exogenous or endogenous modulators of the transcription factors.

DEFINITIONS

A "polynucleotide" is a nucleic acid sequence comprising a plurality of polymerized nucleotide residues, e.g., at least about 15 consecutive polymerized nucleotide residues, optionally at least about 30 consecutive nucleotides, at least about 50 consecutive nucleotides. In many instances, a polynucleotide comprises a nucleotide sequence encoding a polypeptide (or protein) or a domain or fragment thereof. Additionally, the polynucleotide may comprise a promoter, an intron, an enhancer region, a polyadenylation site, a translation initiation

site, 5' or 3' untranslated regions, a reporter gene, a selectable marker, or the like. The polynucleotide can be single stranded or double stranded DNA or RNA. The polynucleotide optionally comprises modified bases or a modified backbone. The polynucleotide can be, e.g., genomic DNA or RNA, a transcript (such as an mRNA), a cDNA, a PCR product, a cloned DNA, 5 a synthetic DNA or RNA, or the like. The polynucleotide can comprise a sequence in either sense or antisense orientations.

A "recombinant polynucleotide" is a polynucleotide that is not in its native state, e.g., the polynucleotide comprises a nucleotide sequence not found in nature, or the polynucleotide is in a context other than that in which it is naturally found, e.g., separated from 10 nucleotide sequences with which it typically is in proximity in nature, or adjacent (or contiguous with) nucleotide sequences with which it typically is not in proximity. For example, the sequence at issue can be cloned into a vector, or otherwise recombined with one or more additional nucleic acid.

An "isolated polynucleotide" is a polynucleotide whether naturally occurring or 15 recombinant, that is present outside the cell in which it is typically found in nature, whether purified or not. Optionally, an isolated polynucleotide is subject to one or more enrichment or purification procedures, e.g., cell lysis, extraction, centrifugation, precipitation, or the like.

A "recombinant polypeptide" is a polypeptide produced by translation of a recombinant polynucleotide. An "isolated polypeptide," whether a naturally occurring or a 20 recombinant polypeptide, is more enriched in (or out of) a cell than the polypeptide in its natural state in a wild type cell, e.g., more than about 5% enriched, more than about 10% enriched, or more than about 20%, or more than about 50%, or more, enriched, i.e., alternatively denoted: 105%, 110%, 120%, 150% or more, enriched relative to wild type standardized at 100%. Such an enrichment is not the result of a natural response of a wild type plant. Alternatively, or 25 additionally, the isolated polypeptide is separated from other cellular components with which it is typically associated, e.g., by any of the various protein purification methods herein.

The term "transgenic plant" refers to a plant that contains genetic material, not found in a wild type plant of the same species, variety or cultivar. The genetic material may include a transgene, an insertional mutagenesis event (such as by transposon or T-DNA 30 insertional mutagenesis), an activation tagging sequence, a mutated sequence, a homologous recombination event or a sequence modified by chimeraplasty. Typically, the foreign genetic material has been introduced into the plant by human manipulation.

A transgenic plant may contain an expression vector or cassette. The expression cassette typically comprises a polypeptide-encoding sequence operably linked (i.e., under

regulatory control of) to appropriate inducible or constitutive regulatory sequences that allow for the expression of polypeptide. The expression cassette can be introduced into a plant by transformation or by breeding after transformation of a parent plant. A plant refers to a whole plant as well as to a plant part, such as seed, fruit, leaf, or root, plant tissue, plant cells or any other plant material, e.g., a plant explant, as well as to progeny thereof, and to *in vitro* systems that mimic biochemical or cellular components or processes in a cell.

The phrase "ectopically expression or altered expression" in reference to a polynucleotide indicates that the pattern of expression in, e.g., a transgenic plant or plant tissue, is different from the expression pattern in a wild type plant or a reference plant of the same species.

For example, the polynucleotide or polypeptide is expressed in a cell or tissue type other than a cell or tissue type in which the sequence is expressed in the wild type plant, or by expression at a time other than at the time the sequence is expressed in the wild type plant, or by a response to different inducible agents, such as hormones or environmental signals, or at different expression levels (either higher or lower) compared with those found in a wild type plant. The term also refers to altered expression patterns that are produced by lowering the levels of expression to below the detection level or completely abolishing expression. The resulting expression pattern can be transient or stable, constitutive or inducible. In reference to a polypeptide, the term "ectopic expression or altered expression" further may relate to altered activity levels resulting from the interactions of the polypeptides with exogenous or endogenous modulators or from interactions with factors or as a result of the chemical modification of the polypeptides.

The term "fragment" or "domain," with respect to a polypeptide, refers to a subsequence of the polypeptide. In some cases, the fragment or domain, is a subsequence of the polypeptide which performs at least one biological function of the intact polypeptide in substantially the same manner, or to a similar extent, as does the intact polypeptide. For example, a polypeptide fragment can comprise a recognizable structural motif or functional domain such as a DNA binding domain that binds to a DNA promoter region, an activation domain or a domain for protein-protein interactions. Fragments can vary in size from as few as 6 amino acids to the full length of the intact polypeptide, but are preferably at least about 30 amino acids in length and more preferably at least about 60 amino acids in length. In reference to a nucleotide sequence, "a fragment" refers to any subsequence of a polynucleotide, typically, of at least consecutive about 15 nucleotides, preferably at least about 30 nucleotides, more preferably at least about 50, of any of the sequences provided herein.

The term "trait" refers to a physiological, morphological, biochemical or physical characteristic of a plant or particular plant material or cell. In some instances, this characteristic

is visible to the human eye, such as seed or plant size, or can be measured by available biochemical techniques, such as the protein, starch or oil content of seed or leaves or by the observation of the expression level of genes, e.g., by employing Northern analysis, RT-PCR, microarray gene expression assays or reporter gene expression systems, or by agricultural observations such as stress tolerance, yield or pathogen tolerance.

“Trait modification” refers to a detectable difference in a characteristic in a plant ectopically expressing a polynucleotide or polypeptide of the present invention relative to a plant not doing so, such as a wild type plant. In some cases, the trait modification can be evaluated quantitatively. For example, the trait modification can entail at least about a 2% increase or decrease in an observed trait (difference), at least a 5% difference, at least about a 10% difference, at least about a 20% difference, at least about a 30%, at least about a 50%, at least about a 70%, or at least about a 100%, or an even greater difference. It is known that there can be a natural variation in the modified trait. Therefore, the trait modification observed entails a change of the normal distribution of the trait in the plants compared with the distribution observed in wild type plant.

Trait modifications of particular interest include those to seed (such as embryo or endosperm), fruit, root, flower, leaf, stem, shoot, seedling or the like, including: enhanced tolerance to environmental conditions including freezing, chilling, heat, drought, water saturation, radiation and ozone; improved tolerance to microbial, fungal or viral diseases; improved tolerance to pest infestations, including nematodes, mollicutes, parasitic higher plants or the like; decreased herbicide sensitivity; improved tolerance of heavy metals or enhanced ability to take up heavy metals; improved growth under poor photoconditions (e.g., low light and/or short day length), or changes in expression levels of genes of interest. Other phenotype that can be modified relate to the production of plant metabolites, such as variations in the production of taxol, tocopherol, tocotrienol, sterols, phytosterols, vitamins, wax monomers, anti-oxidants, amino acids, lignins, cellulose, tannins, prenyl lipids (such as chlorophylls and carotenoids), glucosinolates, and terpenoids, enhanced or compositionally altered protein or oil production (especially in seeds), or modified sugar (insoluble or soluble) and/or starch composition.

Physical plant characteristics that can be modified include cell development (such as the number of trichomes), fruit and seed size and number, yields of plant parts such as stems, leaves and roots, the stability of the seeds during storage, characteristics of the seed pod (e.g., susceptibility to shattering), root hair length and quantity, internode distances, or the quality of seed coat. Plant growth characteristics that can be modified include growth rate, germination rate of seeds, vigor of plants and seedlings, leaf and flower senescence, male sterility, apomixis, flowering time,

flower abscission, rate of nitrogen uptake, biomass or transpiration characteristics, as well as plant architecture characteristics such as apical dominance, branching patterns, number of organs, organ identity, organ shape or size.

POLYPEPTIDES AND POLYNUCLEOTIDES OF THE INVENTION

5 The present invention provides, among other things, transcription factors (TFs), and transcription factor homologue polypeptides, and isolated or recombinant polynucleotides encoding the polypeptides. These polypeptides and polynucleotides may be employed to modify a plant's environmental stress tolerance.

10 Exemplary polynucleotides encoding the polypeptides of the invention were identified in the *Arabidopsis thaliana* GenBank database using publicly available sequence analysis programs and parameters. Sequences initially identified were then further characterized to identify sequences comprising specified sequence strings corresponding to sequence motifs present in families of known transcription factors. Polynucleotide sequences meeting such criteria were confirmed as transcription factors.

15 Additional polynucleotides of the invention were identified by screening *Arabidopsis thaliana* and/or other plant cDNA libraries with probes corresponding to known transcription factors under low stringency hybridization conditions. Additional sequences, including full length coding sequences were subsequently recovered by the rapid amplification of cDNA ends (RACE) procedure, using a commercially available kit according to the
20 manufacturer's instructions. Where necessary, multiple rounds of RACE are performed to isolate 5' and 3' ends. The full length cDNA was then recovered by a routine end-to-end polymerase chain reaction (PCR) using primers specific to the isolated 5' and 3' ends. Exemplary sequences are provided in the Sequence Listing.

25 The polynucleotides of the invention were ectopically expressed in overexpressor or knockout plants and changes in the environmental stress tolerance of the plants was observed. Therefore, the polynucleotides and polypeptides can be employed to improve the environmental stress resistance of plants.

Making polynucleotides

30 The polynucleotides of the invention include sequences that encode transcription factors and transcription factor homologue polypeptides and sequences complementary thereto, as well as unique fragments of coding sequence, or sequence complementary thereto. Such polynucleotides can be, e.g., DNA or RNA, e.g., mRNA, cRNA, synthetic RNA, genomic DNA, cDNA synthetic DNA, oligonucleotides, etc. The polynucleotides are either double-stranded or

single-stranded, and include either, or both sense (i.e., coding) sequences and antisense (i.e., non-coding, complementary) sequences. The polynucleotides include the coding sequence of a transcription factor, or transcription factor homologue polypeptide, in isolation, in combination with additional coding sequences (e.g., a purification tag, a localization signal, as a fusion-protein, as a pre-protein, or the like), in combination with non-coding sequences (e.g., introns or inteins, regulatory elements such as promoters, enhancers, terminators, and the like), and/or in a vector or host environment in which the polynucleotide encoding a transcription factor or transcription factor homologue polypeptide is an endogenous or exogenous gene.

A variety of methods exist for producing the polynucleotides of the invention.

- 10 Procedures for identifying and isolating DNA clones are well known to those of skill in the art, and are described in, e.g., Berger and Kimmel, Guide to Molecular Cloning Techniques, Methods in Enzymology volume 152 Academic Press, Inc., San Diego, CA ("Berger"); Sambrook et al., Molecular Cloning - A Laboratory Manual (2nd Ed.), Vol. 1-3, Cold Spring Harbor Laboratory, Cold Spring Harbor, New York, 1989 ("Sambrook") and Current Protocols in Molecular Biology,
15 F.M. Ausubel et al., eds., Current Protocols, a joint venture between Greene Publishing Associates, Inc. and John Wiley & Sons, Inc., (supplemented through 2000) ("Ausubel").

- Alternatively, polynucleotides of the invention, can be produced by a variety of in vitro amplification methods adapted to the present invention by appropriate selection of specific or degenerate primers. Examples of protocols sufficient to direct persons of skill through
20 in vitro amplification methods, including the polymerase chain reaction (PCR) the ligase chain reaction (LCR), Qbeta-replicase amplification and other RNA polymerase mediated techniques (e.g., NASBA), e.g., for the production of the homologous nucleic acids of the invention are found in Berger, Sambrook, and Ausubel, as well as Mullis et al., (1987) PCR Protocols A Guide to Methods and Applications (Innis et al. eds) Academic Press Inc. San Diego, CA (1990) (Innis).
25 Improved methods for cloning in vitro amplified nucleic acids are described in Wallace et al., U.S. Pat. No. 5,426,039. Improved methods for amplifying large nucleic acids by PCR are summarized in Cheng et al. (1994) Nature 369: 684-685 and the references cited therein, in which PCR amplicons of up to 40kb are generated. One of skill will appreciate that essentially any RNA can be converted into a double stranded DNA suitable for restriction digestion, PCR
30 expansion and sequencing using reverse transcriptase and a polymerase. See, e.g., Ausubel, Sambrook and Berger, *all supra*.

Alternatively, polynucleotides and oligonucleotides of the invention can be assembled from fragments produced by solid-phase synthesis methods. Typically, fragments of up to approximately 100 bases are individually synthesized and then enzymatically or chemically

ligated to produce a desired sequence, e.g., a polynucleotide encoding all or part of a transcription factor. For example, chemical synthesis using the phosphoramidite method is described, e.g., by Beaucage et al. (1981) Tetrahedron Letters 22:1859-69; and Matthes et al. (1984) EMBO J. 3:801-5. According to such methods, oligonucleotides are synthesized, purified, annealed to their complementary strand, ligated and then optionally cloned into suitable vectors. And if so desired, the polynucleotides and polypeptides of the invention can be custom ordered from any of a number of commercial suppliers.

HOMOLOGOUS SEQUENCES

Sequences homologous, i.e., that share significant sequence identity or similarity, to those provided in the Sequence Listing, derived from *Arabidopsis thaliana* or from other plants of choice are also an aspect of the invention. Homologous sequences can be derived from any plant including monocots and dicots and in particular agriculturally important plant species, including but not limited to, crops such as soybean, wheat, corn, potato, cotton, rice, oilseed rape (including canola), sunflower, alfalfa, sugarcane and turf; or fruits and vegetables, such as banana, blackberry, blueberry, strawberry, and raspberry, cantaloupe, carrot, cauliflower, coffee, cucumber, eggplant, grapes, honeydew, lettuce, mango, melon, onion, papaya, peas, peppers, pineapple, spinach, squash, sweet corn, tobacco, tomato, watermelon, rosaceous fruits (such as apple, peach, pear, cherry and plum) and vegetable brassicas (such as broccoli, cabbage, cauliflower, brussel sprouts and kohlrabi). Other crops, fruits and vegetables whose phenotype can be changed include barley, rye, millet, sorghum, currant, avocado, citrus fruits such as oranges, lemons, grapefruit and tangerines, artichoke, cherries, nuts such as the walnut and peanut, endive, leek, roots, such as arrowroot, beet, cassava, turnip, radish, yam, and sweet potato, and beans. The homologous sequences may also be derived from woody species, such as pine, poplar and eucalyptus.

Transcription factors that are homologous to the listed sequences will typically share at least about 30% amino acid sequence identity. More closely related transcription factors can share at least about 50%, about 60%, about 65%, about 70%, about 75% or about 80% or about 90% or about 95% or about 98% or more sequence identity with the listed sequences. Factors that are most closely related to the listed sequences share, e.g., at least about 85%, about 90% or about 95% or more % sequence identity to the listed sequences. At the nucleotide level, the sequences will typically share at least about 40% nucleotide sequence identity, preferably at least about 50%, about 60%, about 70% or about 80% sequence identity, and more preferably about 85%, about 90%, about 95% or about 97% or more sequence identity to one or more of the

listed sequences. The degeneracy of the genetic code enables major variations in the nucleotide sequence of a polynucleotide while maintaining the amino acid sequence of the encoded protein. Conserved domains within a transcription factor family may exhibit a higher degree of sequence homology, such as at least 65% sequence identity including conservative substitutions, and preferably at least 80% sequence identity.

Identifying Nucleic Acids by Hybridization

Polynucleotides homologous to the sequences illustrated in the Sequence Listing can be identified, e.g., by hybridization to each other under stringent or under highly stringent conditions. Single stranded polynucleotides hybridize when they associate based on a variety of well characterized physico-chemical forces, such as hydrogen bonding, solvent exclusion, base stacking and the like. The stringency of a hybridization reflects the degree of sequence identity of the nucleic acids involved, such that the higher the stringency, the more similar are the two polynucleotide strands. Stringency is influenced by a variety of factors, including temperature, salt concentration and composition, organic and non-organic additives, solvents, etc. present in both the hybridization and wash solutions and incubations (and number), as described in more detail in the references cited above.

An example of stringent hybridization conditions for hybridization of complementary nucleic acids which have more than 100 complementary residues on a filter in a Southern or northern blot is about 5°C to 20°C lower than the thermal melting point (T_m) for the specific sequence at a defined ionic strength and pH. The T_m is the temperature (under defined ionic strength and pH) at which 50% of the target sequence hybridizes to a perfectly matched probe. Nucleic acid molecules that hybridize under stringent conditions will typically hybridize to a probe based on either the entire cDNA or selected portions, e.g., to a unique subsequence, of the cDNA under wash conditions of 0.2x SSC to 2.0 x SSC, 0.1% SDS at 50-65° C, for example 0.2 x SSC, 0.1% SDS at 65° C. For identification of less closely related homologues washes can be performed at a lower temperature, e.g., 50° C. In general, stringency is increased by raising the wash temperature and/or decreasing the concentration of SSC.

As another example, stringent conditions can be selected such that an oligonucleotide that is perfectly complementary to the coding oligonucleotide hybridizes to the coding oligonucleotide with at least about a 5-10x higher signal to noise ratio than the ratio for hybridization of the perfectly complementary oligonucleotide to a nucleic acid encoding a transcription factor known as of the filing date of the application. Conditions can be selected such that a higher signal to noise ratio is observed in the particular assay which is used, e.g., about 15x, 25x, 35x, 50x or more. Accordingly, the subject nucleic acid hybridizes to the unique

coding oligonucleotide with at least a 2x higher signal to noise ratio as compared to hybridization of the coding oligonucleotide to a nucleic acid encoding known polypeptide. Again, higher signal to noise ratios can be selected, e.g., about 5x, 10x, 25x, 35x, 50x or more. The particular signal will depend on the label used in the relevant assay, e.g., a fluorescent label, a colorimetric label, a radio active label, or the like.

Alternatively, transcription factor homologue polypeptides can be obtained by screening an expression library using antibodies specific for one or more transcription factors. With the provision herein of the disclosed transcription factor, and transcription factor homologue nucleic acid sequences, the encoded polypeptide(s) can be expressed and purified in a heterologous expression system (e.g., *E. coli*) and used to raise antibodies (monoclonal or polyclonal) specific for the polypeptide(s) in question. Antibodies can also be raised against synthetic peptides derived from transcription factor, or transcription factor homologue, amino acid sequences. Methods of raising antibodies are well known in the art and are described in Harlow and Lane (1988) Antibodies: A Laboratory Manual, Cold Spring Harbor Laboratory, New York. Such antibodies can then be used to screen an expression library produced from the plant from which it is desired to clone additional transcription factor homologues, using the methods described above. The selected cDNAs can be confirmed by sequencing and enzymatic activity.

SEQUENCE VARIATIONS

It will readily be appreciated by those of skill in the art, that any of a variety of polynucleotide sequences are capable of encoding the transcription factors and transcription factor homologue polypeptides of the invention. Due to the degeneracy of the genetic code, many different polynucleotides can encode identical and/or substantially similar polypeptides in addition to those sequences illustrated in the Sequence Listing.

For example, Table 1 illustrates, e.g., that the codons AGC, AGT, TCA, TCC, TCG, and TCT all encode the same amino acid: serine. Accordingly, at each position in the sequence where there is a codon encoding serine, any of the above trinucleotide sequences can be used without altering the encoded polypeptide.

Table 1

Amino acids			Codon							
Alanine	Ala	A	GCA	GCC	GCG	GCU				
Cysteine	Cys	C	TGC	TGT						
Aspartic acid	Asp	D	GAC	GAT						
Glutamic acid	Glu	E	GAA	GAG						
Phenylalanine	Phe	F	TTC	TTT						
Glycine	Gly	G	GGA	GGC	GGG	GGT				
Histidine	His	H	CAC	CAT						
Isoleucine	Ile	I	ATA	ATC	ATT					
Lysine	Lys	K	AAA	AAG						
Leucine	Leu	L	TTA	TTG	CTA	CTC	CTG	CTT		
Methionine	Met	M	ATG							
Asparagine	Asn	N	AAC	AAT						
Proline	Pro	P	CCA	CCC	CCG	CCT				
Glutamine	Gln	Q	CAA	CAG						
Arginine	Arg	R	AGA	AGG	CGA	CGC	CGG	CGT		
Serine	Ser	S	AGC	AGT	TCA	TCC	TCG	TCT		
Threonine	Thr	T	ACA	ACC	ACG	ACT				
Valine	Val	V	GTA	GTC	GTG	GTT				
Tryptophan	Trp	W	TGG							
Tyrosine	Tyr	Y	TAC	TAT						

Sequence alterations that do not change the amino acid sequence encoded by the polynucleotide are termed "silent" variations. With the exception of the codons ATG and TGG, encoding methionine and tryptophan, respectively, any of the possible codons for the same amino acid can be substituted by a variety of techniques, e.g., site-directed mutagenesis, available in the art. Accordingly, any and all such variations of a sequence selected from the above table are a feature of the invention.

In addition to silent variations, other conservative variations that alter one, or a few amino acids in the encoded polypeptide, can be made without altering the function of the polypeptide, these conservative variants are, likewise, a feature of the invention.

For example, substitutions, deletions and insertions introduced into the sequences provided in the Sequence Listing are also envisioned by the invention. Such sequence modifications can be engineered into a sequence by site-directed mutagenesis (Wu (ed.) Meth. Enzymol. (1993) vol. 217, Academic Press) or the other methods noted below. Amino acid substitutions are typically of single residues; insertions usually will be on the order of about from 1 to 10 amino acid residues; and deletions will range about from 1 to 30 residues. In preferred embodiments, deletions or insertions are made in adjacent pairs, e.g., a deletion of two residues or insertion of two residues. Substitutions, deletions, insertions or any combination thereof can be

combined to arrive at a sequence. The mutations that are made in the polynucleotide encoding the transcription factor should not place the sequence out of reading frame and should not create complementary regions that could produce secondary mRNA structure. Preferably, the polypeptide encoded by the DNA performs the desired function.

5 Conservative substitutions are those in which at least one residue in the amino acid sequence has been removed and a different residue inserted in its place. Such substitutions generally are made in accordance with the Table 2 when it is desired to maintain the activity of the protein. Table 2 shows amino acids which can be substituted for an amino acid in a protein and which are typically regarded as conservative substitutions.

10

Table 2

Residue	Conservative Substitutions
Ala	Ser
Arg	Lys
Asn	Gln; His
Asp	Glu
Gln	Asn
Cys	Ser
Glu	Asp
Gly	Pro
His	Asn; Gln
Ile	Leu, Val
Leu	Ile; Val
Lys	Arg; Gln
Met	Leu; Ile
Phe	Met; Leu; Tyr
Ser	Thr; Gly
Thr	Ser; Val
Trp	Tyr
Tyr	Trp; Phe
Val	Ile; Leu

Substitutions that are less conservative than those in Table 2 can be selected by picking residues that differ more significantly in their effect on maintaining (a) the structure of

the polypeptide backbone in the area of the substitution, for example, as a sheet or helical conformation, (b) the charge or hydrophobicity of the molecule at the target site, or (c) the bulk of the side chain. The substitutions which in general are expected to produce the greatest changes in protein properties will be those in which (a) a hydrophilic residue, e.g., seryl or threonyl, is substituted for (or by) a hydrophobic residue, e.g., leucyl, isoleucyl, phenylalanyl, valyl or alanyl; (b) a cysteine or proline is substituted for (or by) any other residue; (c) a residue having an electropositive side chain, e.g., lysyl, arginyl, or histidyl, is substituted for (or by) an electronegative residue, e.g., glutamyl or aspartyl; or (d) a residue having a bulky side chain, e.g., phenylalanine, is substituted for (or by) one not having a side chain, e.g., glycine.

10 FURTHER MODIFYING SEQUENCES OF THE INVENTION—MUTATION/ FORCED EVOLUTION

In addition to generating silent or conservative substitutions as noted, above, the present invention optionally includes methods of modifying the sequences of the Sequence Listing. In the methods, nucleic acid or protein modification methods are used to alter the given sequences to produce new sequences and/or to chemically or enzymatically modify given sequences to change the properties of the nucleic acids or proteins.

Thus, in one embodiment, given nucleic acid sequences are modified, e.g., according to standard mutagenesis or artificial evolution methods to produce modified sequences. For example, Ausubel, *supra*, provides additional details on mutagenesis methods. Artificial forced evolution methods are described, e.g., by Stemmer (1994) *Nature* 370:389-391, and Stemmer (1994) *Proc. Natl. Acad. Sci. USA* 91:10747-10751. Many other mutation and evolution methods are also available and expected to be within the skill of the practitioner.

Similarly, chemical or enzymatic alteration of expressed nucleic acids and polypeptides can be performed by standard methods. For example, sequence can be modified by addition of lipids, sugars, peptides, organic or inorganic compounds, by the inclusion of modified nucleotides or amino acids, or the like. For example, protein modification techniques are illustrated in Ausubel, *supra*. Further details on chemical and enzymatic modifications can be found herein. These modification methods can be used to modify any given sequence, or to modify any sequence produced by the various mutation and artificial evolution modification methods noted herein.

Accordingly, the invention provides for modification of any given nucleic acid by mutation, evolution, chemical or enzymatic modification, or other available methods, as well as for the products produced by practicing such methods, e.g., using the sequences herein as a starting substrate for the various modification approaches.

For example, optimized coding sequence containing codons preferred by a particular prokaryotic or eukaryotic host can be used e.g., to increase the rate of translation or to produce recombinant RNA transcripts having desirable properties, such as a longer half-life, as compared with transcripts produced using a non-optimized sequence. Translation stop codons can also be modified to reflect host preference. For example, preferred stop codons for *S. cerevisiae* and mammals are TAA and TGA, respectively. The preferred stop codon for monocotyledonous plants is TGA, whereas insects and *E. coli* prefer to use TAA as the stop codon.

The polynucleotide sequences of the present invention can also be engineered in order to alter a coding sequence for a variety of reasons, including but not limited to, alterations which modify the sequence to facilitate cloning, processing and/or expression of the gene product. For example, alterations are optionally introduced using techniques which are well known in the art, e.g., site-directed mutagenesis, to insert new restriction sites, to alter glycosylation patterns, to change codon preference, to introduce splice sites, etc.

Furthermore, a fragment or domain derived from any of the polypeptides of the invention can be combined with domains derived from other transcription factors or synthetic domains to modify the biological activity of a transcription factor. For instance, a DNA binding domain derived from a transcription factor of the invention can be combined with the activation domain of another transcription factor or with a synthetic activation domain. A transcription activation domain assists in initiating transcription from a DNA binding site. Examples include the transcription activation region of VP16 or GAL4 (Moore et al. (1998) Proc. Natl. Acad. Sci. USA 95: 376-381; and Aoyama et al. (1995) Plant Cell 7:1773-1785), peptides derived from bacterial sequences (Ma and Ptashne (1987) Cell 51; 113-119) and synthetic peptides (Giniger and Ptashne, (1987) Nature 330:670-672).

EXPRESSION AND MODIFICATION OF POLYPEPTIDES

Typically, polynucleotide sequences of the invention are incorporated into recombinant DNA (or RNA) molecules that direct expression of polypeptides of the invention in appropriate host cells, transgenic plants, in vitro translation systems, or the like. Due to the inherent degeneracy of the genetic code, nucleic acid sequences which encode substantially the same or a functionally equivalent amino acid sequence can be substituted for any listed sequence to provide for cloning and expressing the relevant homologue.

Vectors, Promoters and Expression Systems

The present invention includes recombinant constructs comprising one or more of the nucleic acid sequences herein. The constructs typically comprise a vector, such as a plasmid, a cosmid, a phage, a virus (e.g., a plant virus), a bacterial artificial chromosome (BAC),
5 a yeast artificial chromosome (YAC), or the like, into which a nucleic acid sequence of the invention has been inserted, in a forward or reverse orientation. In a preferred aspect of this embodiment, the construct further comprises regulatory sequences, including, for example, a promoter, operably linked to the sequence. Large numbers of suitable vectors and promoters are known to those of skill in the art, and are commercially available.

10 General texts which describe molecular biological techniques useful herein, including the use and production of vectors, promoters and many other relevant topics, include Berger, Sambrook and Ausubel, *supra*. Any of the identified sequences can be incorporated into a cassette or vector, e.g., for expression in plants. A number of expression vectors suitable for stable transformation of plant cells or for the establishment of transgenic plants have been described
15 including those described in Weissbach and Weissbach, (1989) Methods for Plant Molecular Biology, Academic Press, and Gelvin et al., (1990) Plant Molecular Biology Manual, Kluwer Academic Publishers. Specific examples include those derived from a Ti plasmid of *Agrobacterium tumefaciens*, as well as those disclosed by Herrera-Estrella et al. (1983) Nature 303: 209, Bevan (1984) Nucl Acid Res. 12: 8711-8721, Klee (1985) Bio/Technology 3: 637-642,
20 for dicotyledonous plants.

Alternatively, non-Ti vectors can be used to transfer the DNA into monocotyledonous plants and cells by using free DNA delivery techniques. Such methods can involve, for example, the use of liposomes, electroporation, microprojectile bombardment, silicon
25 carbide whiskers, and viruses. By using these methods transgenic plants such as wheat, rice (Christou (1991) Bio/Technology 9: 957-962) and corn (Gordon-Kamm (1990) Plant Cell 2: 603-618) can be produced. An immature embryo can also be a good target tissue for monocots for direct DNA delivery techniques by using the particle gun (Weeks et al. (1993) Plant Physiol 102: 1077-1084; Vasil (1993) Bio/Technology 10: 667-674; Wan and Lemeaux (1994) Plant Physiol 104: 37-48, and for *Agrobacterium*-mediated DNA transfer (Ishida et al. (1996) Nature Biotech
30 14: 745-750).

Typically, plant transformation vectors include one or more cloned plant coding sequence (genomic or cDNA) under the transcriptional control of 5' and 3' regulatory sequences and a dominant selectable marker. Such plant transformation vectors typically also contain a promoter (e.g., a regulatory region controlling inducible or constitutive, environmentally-or

developmentally-regulated, or cell- or tissue-specific expression), a transcription initiation start site, an RNA processing signal (such as intron splice sites), a transcription termination site, and/or a polyadenylation signal.

Examples of constitutive plant promoters which can be useful for expressing the
 5 TF sequence include: the cauliflower mosaic virus (CaMV) 35S promoter, which confers constitutive, high-level expression in most plant tissues (*see, e.g.,* Odel et al. (1985) Nature 313:810); the nopaline synthase promoter (An et al. (1988) Plant Physiol 88:547); and the octopine synthase promoter (Fromm et al. (1989) Plant Cell 1: 977).

A variety of plant gene promoters that regulate gene expression in response to
 10 environmental, hormonal, chemical, developmental signals, and in a tissue-active manner can be used for expression of a TF sequence in plants. Choice of a promoter is based largely on the phenotype of interest and is determined by such factors as tissue (e.g., seed, fruit, root, pollen, vascular tissue, flower, carpel, etc.), inducibility (e.g., in response to wounding, heat, cold, drought, light, pathogens, etc.), timing, developmental stage, and the like. Numerous known
 15 promoters have been characterized and can favorably be employed to promote expression of a polynucleotide of the invention in a transgenic plant or cell of interest. For example, tissue specific promoters include: seed-specific promoters (such as the napin, phaseolin or DC3 promoter described in US Pat. No. 5,773,697), fruit-specific promoters that are active during fruit ripening (such as the dru 1 promoter (US Pat. No. 5,783,393), or the 2A11 promoter (US Pat. No.
 20 4,943,674) and the tomato polygalacturonase promoter (Bird et al. (1988) Plant Mol Biol 11:651), root-specific promoters, such as those disclosed in US Patent Nos. 5,618,988, 5,837,848 and 5,905,186, pollen-active promoters such as PTA29, PTA26 and PTA13 (US Pat. No. 5,792,929), promoters active in vascular tissue (Ringli and Keller (1998) Plant Mol Biol 37:977-988), flower-specific (Kaiser et al. (1995) Plant Mol Biol 28:231-243), pollen (Baerson et al. (1994) Plant Mol
 25 Biol 26:1947-1959), carpels (Ohl et al. (1990) Plant Cell 2:837-848), pollen and ovules (Baerson et al. (1993) Plant Mol Biol 22:255-267), auxin-inducible promoters (such as that described in van der Kop et al. (1999) Plant Mol Biol 39:979-990 or Baumann et al. (1999) Plant Cell 11:323-334), cytokinin-inducible promoter (Guevara-Garcia (1998) Plant Mol Biol 38:743-753), promoters responsive to gibberellin (Shi et al. (1998) Plant Mol Biol 38:1053-1060, Willmott et
 30 al. (1998) 38:817-825) and the like. Additional promoters are those that elicit expression in response to heat (Ainley et al. (1993) Plant Mol Biol 22: 13-23), light (e.g., the pea rbcS-3A promoter, Kuhlemeier et al. (1989) Plant Cell 1:471, and the maize rbcS promoter, Schaffner and Sheen (1991) Plant Cell 3: 997); wounding (e.g., *wun1*, Siebertz et al. (1989) Plant Cell 1: 961); pathogens (such as the PR-1 promoter described in Buchel et al. (1999) Plant Mol. Biol. 40:387-

396, and the PDF1.2 promoter described in Manners et al. (1998) Plant Mol. Biol. 38:1071-80), and chemicals such as methyl jasmonate or salicylic acid (Gatz et al. (1997) Plant Mol Biol 48: 89-108). In addition, the timing of the expression can be controlled by using promoters such as those acting at senescence (An and Amazon (1995) Science 270: 1986-1988); or late seed development (Odell et al. (1994) Plant Physiol 106:447-458).

Plant expression vectors can also include RNA processing signals that can be positioned within, upstream or downstream of the coding sequence. In addition, the expression vectors can include additional regulatory sequences from the 3'-untranslated region of plant genes, e.g., a 3' terminator region to increase mRNA stability of the mRNA, such as the PI-II terminator region of potato or the octopine or nopaline synthase 3' terminator regions.

Additional Expression Elements

Specific initiation signals can aid in efficient translation of coding sequences.

These signals can include, e.g., the ATG initiation codon and adjacent sequences. In cases where a coding sequence, its initiation codon and upstream sequences are inserted into the appropriate expression vector, no additional translational control signals may be needed. However, in cases where only coding sequence (e.g., a mature protein coding sequence), or a portion thereof, is inserted, exogenous transcriptional control signals including the ATG initiation codon can be separately provided. The initiation codon is provided in the correct reading frame to facilitate transcription. Exogenous transcriptional elements and initiation codons can be of various origins, both natural and synthetic. The efficiency of expression can be enhanced by the inclusion of enhancers appropriate to the cell system in use.

Expression Hosts

The present invention also relates to host cells which are transduced with vectors of the invention, and the production of polypeptides of the invention (including fragments thereof) by recombinant techniques. Host cells are genetically engineered (i.e., nucleic acids are introduced, e.g., transduced, transformed or transfected) with the vectors of this invention, which may be, for example, a cloning vector or an expression vector comprising the relevant nucleic acids herein. The vector is optionally a plasmid, a viral particle, a phage, a naked nucleic acids, *etc.* The engineered host cells can be cultured in conventional nutrient media modified as appropriate for activating promoters, selecting transformants, or amplifying the relevant gene. The culture conditions, such as temperature, pH and the like, are those previously used with the host cell selected for expression, and will be apparent to those skilled in the art and in the references cited herein, including, Sambrook and Ausubel.

The host cell can be a eukaryotic cell, such as a yeast cell, or a plant cell, or the host cell can be a prokaryotic cell, such as a bacterial cell. Plant protoplasts are also suitable for some applications. For example, the DNA fragments are introduced into plant tissues, cultured plant cells or plant protoplasts by standard methods including electroporation (Fromm et al., (1985) Proc. Natl. Acad. Sci. USA 82, 5824, infection by viral vectors such as cauliflower mosaic virus (CaMV) (Hohn et al., (1982) Molecular Biology of Plant Tumors, (Academic Press, New York) pp. 549-560; US 4,407,956), high velocity ballistic penetration by small particles with the nucleic acid either within the matrix of small beads or particles, or on the surface (Klein et al., (1987) Nature 327, 70-73), use of pollen as vector (WO 85/01856), or use of *Agrobacterium tumefaciens* or *A. rhizogenes* carrying a T-DNA plasmid in which DNA fragments are cloned. The T-DNA plasmid is transmitted to plant cells upon infection by *Agrobacterium tumefaciens*, and a portion is stably integrated into the plant genome (Horsch et al. (1984) Science 233:496-498; Fraley et al. (1983) Proc. Natl. Acad. Sci. USA 80, 4803).

The cell can include a nucleic acid of the invention which encodes a polypeptide, wherein the cells expresses a polypeptide of the invention. The cell can also include vector sequences, or the like. Furthermore, cells and transgenic plants which include any polypeptide or nucleic acid above or throughout this specification, e.g., produced by transduction of a vector of the invention, are an additional feature of the invention.

For long-term, high-yield production of recombinant proteins, stable expression can be used. Host cells transformed with a nucleotide sequence encoding a polypeptide of the invention are optionally cultured under conditions suitable for the expression and recovery of the encoded protein from cell culture. The protein or fragment thereof produced by a recombinant cell may be secreted, membrane-bound, or contained intracellularly, depending on the sequence and/or the vector used. As will be understood by those of skill in the art, expression vectors containing polynucleotides encoding mature proteins of the invention can be designed with signal sequences which direct secretion of the mature polypeptides through a prokaryotic or eukaryotic cell membrane.

Modified Amino Acids

Polypeptides of the invention may contain one or more modified amino acids.

The presence of modified amino acids may be advantageous in, for example, increasing polypeptide half-life, reducing polypeptide antigenicity or toxicity, increasing polypeptide storage stability, or the like. Amino acid(s) are modified, for example, co-translationally or post-translationally during recombinant production or modified by synthetic or chemical means.

Non-limiting examples of a modified amino acid include incorporation or other use of acetylated amino acids, glycosylated amino acids, sulfated amino acids, prenylated (e.g., farnesylated, geranylgeranylated) amino acids, PEG modified (e.g., "PEGylated") amino acids, biotinylated amino acids, carboxylated amino acids, phosphorylated amino acids, etc. References
5 adequate to guide one of skill in the modification of amino acids are replete throughout the literature.

IDENTIFICATION OF ADDITIONAL FACTORS

A transcription factor provided by the present invention can also be used to identify additional endogenous or exogenous molecules that can affect a phenotype or trait of
10 interest. On the one hand, such molecules include organic (small or large molecules) and/or inorganic compounds that affect expression of (i.e., regulate) a particular transcription factor. Alternatively, such molecules include endogenous molecules that are acted upon either at a transcriptional level by a transcription factor of the invention to modify a phenotype as desired. For example, the transcription factors can be employed to identify one or more downstream gene
15 with which is subject to a regulatory effect of the transcription factor. In one approach, a transcription factor or transcription factor homologue of the invention is expressed in a host cell, e.g., a transgenic plant cell, tissue or explant, and expression products, either RNA or protein, of likely or random targets are monitored, e.g., by hybridization to a microarray of nucleic acid probes corresponding to genes expressed in a tissue or cell type of interest, by two-dimensional
20 gel electrophoresis of protein products, or by any other method known in the art for assessing expression of gene products at the level of RNA or protein. Alternatively, a transcription factor of the invention can be used to identify promoter sequences (i.e., binding sites) involved in the regulation of a downstream target. After identifying a promoter sequence, interactions between the transcription factor and the promoter sequence can be modified by changing specific
25 nucleotides in the promoter sequence or specific amino acids in the transcription factor that interact with the promoter sequence to alter a plant trait. Typically, transcription factor DNA binding sites are identified by gel shift assays. After identifying the promoter regions, the promoter region sequences can be employed in double-stranded DNA arrays to identify molecules that affect the interactions of the transcription factors with their promoters (Bulyk et al.
30 (1999) Nature Biotechnology 17:573-577).

The identified transcription factors are also useful to identify proteins that modify the activity of the transcription factor. Such modification can occur by covalent modification, such as by phosphorylation, or by protein-protein (homo or-heteropolymer) interactions. Any

method suitable for detecting protein-protein interactions can be employed. Among the methods that can be employed are co-immunoprecipitation, cross-linking and co-purification through gradients or chromatographic columns, and the two-hybrid yeast system.

The two-hybrid system detects protein interactions in vivo and is described in

5 Chien, et al., (1991), Proc. Natl. Acad. Sci. USA 88, 9578-9582 and is commercially available from Clontech (Palo Alto, Calif.). In such a system, plasmids are constructed that encode two hybrid proteins: one consists of the DNA-binding domain of a transcription activator protein fused to the TF polypeptide and the other consists of the transcription activator protein's activation domain fused to an unknown protein that is encoded by a cDNA that has been
10 recombined into the plasmid as part of a cDNA library. The DNA-binding domain fusion plasmid and the cDNA library are transformed into a strain of the yeast *Saccharomyces cerevisiae* that contains a reporter gene (e.g., lacZ) whose regulatory region contains the transcription activator's binding site. Either hybrid protein alone cannot activate transcription of the reporter gene. Interaction of the two hybrid proteins reconstitutes the functional activator protein and results in
15 expression of the reporter gene, which is detected by an assay for the reporter gene product. Then, the library plasmids responsible for reporter gene expression are isolated and sequenced to identify the proteins encoded by the library plasmids. After identifying proteins that interact with the transcription factors, assays for compounds that interfere with the TF protein-protein interactions can be preformed.

20 IDENTIFICATION OF MODULATORS

In addition to the intracellular molecules described above, extracellular molecules that alter activity or expression of a transcription factor, either directly or indirectly, can be identified. For example, the methods can entail first placing a candidate molecule in contact with a plant or plant cell. The molecule can be introduced by topical administration, such
25 as spraying or soaking of a plant, and then the molecule's effect on the expression or activity of the TF polypeptide or the expression of the polynucleotide monitored. Changes in the expression of the TF polypeptide can be monitored by use of polyclonal or monoclonal antibodies, gel electrophoresis or the like. Changes in the expression of the corresponding polynucleotide sequence can be detected by use of microarrays, Northernblots, quantitative PCR, or any other
30 technique for monitoring changes in mRNA expression. These techniques are exemplified in Ausubel et al. (eds) Current Protocols in Molecular Biology, John Wiley & Sons (1998). Such changes in the expression levels can be correlated with modified plant traits and thus identified

molecules can be useful for soaking or spraying on fruit, vegetable and grain crops to modify traits in plants.

Essentially any available composition can be tested for modulatory activity of expression or activity of any nucleic acid or polypeptide herein. Thus, available libraries of compounds such as chemicals, polypeptides, nucleic acids and the like can be tested for modulatory activity. Often, potential modulator compounds can be dissolved in aqueous or organic (e.g., DMSO-based) solutions for easy delivery to the cell or plant of interest in which the activity of the modulator is to be tested. Optionally, the assays are designed to screen large modulator composition libraries by automating the assay steps and providing compounds from any convenient source to assays, which are typically run in parallel (e.g., in microtiter formats on microtiter plates in robotic assays).

In one embodiment, high throughput screening methods involve providing a combinatorial library containing a large number of potential compounds (potential modulator compounds). Such "combinatorial chemical libraries" are then screened in one or more assays, as described herein, to identify those library members (particular chemical species or subclasses) that display a desired characteristic activity. The compounds thus identified can serve as target compounds.

A combinatorial chemical library can be, e.g., a collection of diverse chemical compounds generated by chemical synthesis or biological synthesis. For example, a combinatorial chemical library such as a polypeptide library is formed by combining a set of chemical building blocks (e.g., in one example, amino acids) in every possible way for a given compound length (i.e., the number of amino acids in a polypeptide compound of a set length). Exemplary libraries include peptide libraries, nucleic acid libraries, antibody libraries (see, e.g., Vaughn et al. (1996) Nature Biotechnology, 14(3):309-314 and PCT/US96/10287), carbohydrate libraries (see, e.g., Liang et al. Science (1996) 274:1520-1522 and U.S. Patent 5,593,853), peptide nucleic acid libraries (see, e.g., U.S. Patent 5,539,083), and small organic molecule libraries (see, e.g., benzodiazepines, Baum C&EN Jan 18, page 33 (1993); isoprenoids, U.S. Patent 5,569,588; thiazolidinones and metathiazanones, U.S. Patent 5,549,974; pyrrolidines, U.S. Patents 5,525,735 and 5,519,134; morpholino compounds, U.S. Patent 5,506,337) and the like.

Preparation and screening of combinatorial or other libraries is well known to those of skill in the art. Such combinatorial chemical libraries include, but are not limited to, peptide libraries (see, e.g., U.S. Patent 5,010,175, Furka, Int. J. Pept. Prot. Res. 37:487-493 (1991) and Houghton et al. Nature 354:84-88 (1991)). Other chemistries for generating chemical diversity libraries can also be used.

In addition, as noted, compound screening equipment for high-throughput screening is generally available, e.g., using any of a number of well known robotic systems that have also been developed for solution phase chemistries useful in assay systems. These systems include automated workstations including an automated synthesis apparatus and robotic systems utilizing robotic arms. Any of the above devices are suitable for use with the present invention, e.g., for high-throughput screening of potential modulators. The nature and implementation of modifications to these devices (if any) so that they can operate as discussed herein will be apparent to persons skilled in the relevant art.

Indeed, entire high throughput screening systems are commercially available. These systems typically automate entire procedures including all sample and reagent pipetting, liquid dispensing, timed incubations, and final readings of the microplate in detector(s) appropriate for the assay. These configurable systems provide high throughput and rapid start up as well as a high degree of flexibility and customization. Similarly, microfluidic implementations of screening are also commercially available.

The manufacturers of such systems provide detailed protocols the various high throughput. Thus, for example, Zymark Corp. provides technical bulletins describing screening systems for detecting the modulation of gene transcription, ligand binding, and the like. The integrated systems herein, in addition to providing for sequence alignment and, optionally, synthesis of relevant nucleic acids, can include such screening apparatus to identify modulators that have an effect on one or more polynucleotides or polypeptides according to the present invention.

In some assays it is desirable to have positive controls to ensure that the components of the assays are working properly. At least two types of positive controls are appropriate. That is, known transcriptional activators or inhibitors can be incubated with cells/plants/ etc. in one sample of the assay, and the resulting increase/decrease in transcription can be detected by measuring the resulting increase in RNA/ protein expression, etc., according to the methods herein. It will be appreciated that modulators can also be combined with transcriptional activators or inhibitors to find modulators which inhibit transcriptional activation or transcriptional repression. Either expression of the nucleic acids and proteins herein or any additional nucleic acids or proteins activated by the nucleic acids or proteins herein, or both, can be monitored.

In an embodiment, the invention provides a method for identifying compositions that modulate the activity or expression of a polynucleotide or polypeptide of the invention. For example, a test compound, whether a small or large molecule, is placed in contact with a cell,

plant (or plant tissue or explant), or composition comprising the polynucleotide or polypeptide of interest and a resulting effect on the cell, plant, (or tissue or explant) or composition is evaluated by monitoring, either directly or indirectly, one or more of: expression level of the polynucleotide or polypeptide, activity (or modulation of the activity) of the polynucleotide or polypeptide. In some cases, an alteration in a plant phenotype can be detected following contact of a plant (or plant cell, or tissue or explant) with the putative modulator, e.g., by modulation of expression or activity of a polynucleotide or polypeptide of the invention.

SUBSEQUENCES

Also contemplated are uses of polynucleotides, also referred to herein as oligonucleotides, typically having at least 12 bases, preferably at least 15, more preferably at least 20, 30, or 50 bases, which hybridize under at least highly stringent (or ultra-high stringent or ultra-ultra- high stringent conditions) conditions to a polynucleotide sequence described above. The polynucleotides may be used as probes, primers, sense and antisense agents, and the like, according to methods as noted *supra*.

Subsequences of the polynucleotides of the invention, including polynucleotide fragments and oligonucleotides are useful as nucleic acid probes and primers. An oligonucleotide suitable for use as a probe or primer is at least about 15 nucleotides in length, more often at least about 18 nucleotides, often at least about 21 nucleotides, frequently at least about 30 nucleotides, or about 40 nucleotides, or more in length. A nucleic acid probe is useful in hybridization protocols, e.g., to identify additional polypeptide homologues of the invention, including protocols for microarray experiments. Primers can be annealed to a complementary target DNA strand by nucleic acid hybridization to form a hybrid between the primer and the target DNA strand, and then extended along the target DNA strand by a DNA polymerase enzyme. Primer pairs can be used for amplification of a nucleic acid sequence, e.g., by the polymerase chain reaction (PCR) or other nucleic-acid amplification methods. See Sambrook and Ausubel, *supra*.

In addition, the invention includes an isolated or recombinant polypeptide including a subsequence of at least about 15 contiguous amino acids encoded by the recombinant or isolated polynucleotides of the invention. For example, such polypeptides, or domains or fragments thereof, can be used as immunogens, e.g., to produce antibodies specific for the polypeptide sequence, or as probes for detecting a sequence of interest. A subsequence can range in size from about 15 amino acids in length up to and including the full length of the polypeptide.

PRODUCTION OF TRANSGENIC PLANTS

Modification of Traits

The polynucleotides of the invention are favorably employed to produce transgenic plants with various traits, or characteristics, that have been modified in a desirable manner, e.g., to improve the environmental stress resistance of a plant. For example, alteration of expression levels or patterns (e.g., spatial or temporal expression patterns) of one or more of the transcription factors (or transcription factor homologues) of the invention, as compared with the levels of the same protein found in a wild type plant, can be used to modify a plant's traits. An illustrative example of trait modification, improved environmental stress tolerance, by altering expression levels of a particular transcription factor is described further in the Examples and the Sequence Listing.

Antisense and Cosuppression Approaches

In addition to expression of the nucleic acids of the invention as gene replacement or plant phenotype modification nucleic acids, the nucleic acids are also useful for sense and anti-sense suppression of expression, e.g., to down-regulate expression of a nucleic acid of the invention, e.g., as a further mechanism for modulating plant phenotype. That is, the nucleic acids of the invention, or subsequences or anti-sense sequences thereof, can be used to block expression of naturally occurring homologous nucleic acids. A variety of sense and anti-sense technologies are known in the art, e.g., as set forth in Lichtenstein and Nellen (1997)

Antisense Technology: A Practical Approach IRL Press at Oxford University, Oxford, England. In general, sense or anti-sense sequences are introduced into a cell, where they are optionally amplified, e.g., by transcription. Such sequences include both simple oligonucleotide sequences and catalytic sequences such as ribozymes.

For example, a reduction or elimination of expression (i.e., a "knock-out") of a transcription factor or transcription factor homologue polypeptide in a transgenic plant, e.g., to modify a plant trait, can be obtained by introducing an antisense construct corresponding to the polypeptide of interest as a cDNA. For antisense suppression, the transcription factor or homologue cDNA is arranged in reverse orientation (with respect to the coding sequence) relative to the promoter sequence in the expression vector. The introduced sequence need not be the full length cDNA or gene, and need not be identical to the cDNA or gene found in the plant type to be transformed. Typically, the antisense sequence need only be capable of hybridizing to the target gene or RNA of interest. Thus, where the introduced sequence is of shorter length, a higher degree of homology to the endogenous transcription factor sequence will be needed for effective antisense suppression. While antisense sequences of various lengths can be utilized, preferably,

the introduced antisense sequence in the vector will be at least 30 nucleotides in length, and improved antisense suppression will typically be observed as the length of the antisense sequence increases. Preferably, the length of the antisense sequence in the vector will be greater than 100 nucleotides. Transcription of an antisense construct as described results in the production of RNA molecules that are the reverse complement of mRNA molecules transcribed from the endogenous transcription factor gene in the plant cell.

Suppression of endogenous transcription factor gene expression can also be achieved using a ribozyme. Ribozymes are RNA molecules that possess highly specific endoribonuclease activity. The production and use of ribozymes are disclosed in U.S. Patent No. 4,987,071 and U.S. Patent No. 5,543,508. Synthetic ribozyme sequences including antisense RNAs can be used to confer RNA cleaving activity on the antisense RNA, such that endogenous mRNA molecules that hybridize to the antisense RNA are cleaved, which in turn leads to an enhanced antisense inhibition of endogenous gene expression.

Vectors in which RNA encoded by a transcription factor or transcription factor homologue cDNA is over-expressed can also be used to obtain co-suppression of a corresponding endogenous gene, e.g., in the manner described in U.S. Patent No. 5,231,020 to Jorgensen. Such co-suppression (also termed sense suppression) does not require that the entire transcription factor cDNA be introduced into the plant cells, nor does it require that the introduced sequence be exactly identical to the endogenous transcription factor gene of interest. However, as with antisense suppression, the suppressive efficiency will be enhanced as specificity of hybridization is increased, e.g., as the introduced sequence is lengthened, and/or as the sequence similarity between the introduced sequence and the endogenous transcription factor gene is increased.

Vectors expressing an untranslatable form of the transcription factor mRNA, e.g., sequences comprising one or more stop codon, or nonsense mutation) can also be used to suppress expression of an endogenous transcription factor, thereby reducing or eliminating its activity and modifying one or more traits. Methods for producing such constructs are described in U.S. Patent No. 5,583,021. Preferably, such constructs are made by introducing a premature stop codon into the transcription factor gene. Alternatively, a plant trait can be modified by gene silencing using double-strand RNA (Sharp (1999) Genes and Development 13: 139-141).

Another method for abolishing the expression of a gene is by insertion mutagenesis using the T-DNA of *Agrobacterium tumefaciens*. After generating the insertion mutants, the mutants can be screened to identify those containing the insertion in a transcription factor or transcription factor homologue gene. Plants containing a single transgene insertion

event at the desired gene can be crossed to generate homozygous plants for the mutation (Koncz et al. (1992) Methods in Arabidopsis Research, World Scientific).

Alternatively, a plant phenotype can be altered by eliminating an endogenous gene, such as a transcription factor or transcription factor homologue, e.g., by homologous recombination (Kempin et al. (1997) Nature 389:802).

A plant trait can also be modified by using the cre-lox system (for example, as described in US Pat. No. 5,658,772). A plant genome can be modified to include first and second lox sites that are then contacted with a Cre recombinase. If the lox sites are in the same orientation, the intervening DNA sequence between the two sites is excised. If the lox sites are in the opposite orientation, the intervening sequence is inverted.

The polynucleotides and polypeptides of this invention can also be expressed in a plant in the absence of an expression cassette by manipulating the activity or expression level of the endogenous gene by other means. For example, by ectopically expressing a gene by T-DNA activation tagging (Ichikawa et al. (1997) Nature 390 698-701; Kakimoto et al. (1996) Science 274: 982-985). This method entails transforming a plant with a gene tag containing multiple transcriptional enhancers and once the tag has inserted into the genome, expression of a flanking gene coding sequence becomes deregulated. In another example, the transcriptional machinery in a plant can be modified so as to increase transcription levels of a polynucleotide of the invention (See, e.g., PCT Publications WO 96/06166 and WO 98/53057 which describe the modification of the DNA binding specificity of zinc finger proteins by changing particular amino acids in the DNA binding motif).

The transgenic plant can also include the machinery necessary for expressing or altering the activity of a polypeptide encoded by an endogenous gene, for example by altering the phosphorylation state of the polypeptide to maintain it in an activated state.

Transgenic plants (or plant cells, or plant explants, or plant tissues) incorporating the polynucleotides of the invention and/or expressing the polypeptides of the invention can be produced by a variety of well established techniques as described above. Following construction of a vector, most typically an expression cassette, including a polynucleotide, e.g., encoding a transcription factor or transcription factor homologue, of the invention, standard techniques can be used to introduce the polynucleotide into a plant, a plant cell, a plant explant or a plant tissue of interest. Optionally, the plant cell, explant or tissue can be regenerated to produce a transgenic plant.

The plant can be any higher plant, including gymnosperms, monocotyledonous and dicotyledonous plants. Suitable protocols are available for *Leguminosae* (alfalfa, soybean,

clover, etc.), *Umbelliferae* (carrot, celery, parsnip), *Cruciferae* (cabbage, radish, rapeseed, broccoli, etc.), *Curcubitaceae* (melons and cucumber), *Gramineae* (wheat, corn, rice, barley, millet, etc.), *Solanaceae* (potato, tomato, tobacco, peppers, etc.), and various other crops. See protocols described in Ammirato et al. (1984) Handbook of Plant Cell Culture –Crop Species.

- 5 Macmillan Publ. Co. Shimamoto et al. (1989) Nature 338:274-276; Fromm et al. (1990) Bio/Technology 8:833-839; and Vasil et al. (1990) Bio/Technology 8:429-434.

Transformation and regeneration of both monocotyledonous and dicotyledonous plant cells is now routine, and the selection of the most appropriate transformation technique will be determined by the practitioner. The choice of method will vary with the type of plant to be
10 transformed; those skilled in the art will recognize the suitability of particular methods for given plant types. Suitable methods can include, but are not limited to: electroporation of plant protoplasts; liposome-mediated transformation; polyethylene glycol (PEG) mediated transformation; transformation using viruses; micro-injection of plant cells; micro-projectile bombardment of plant cells; vacuum infiltration; and *Agrobacterium tumefaciens* mediated
15 transformation. Transformation means introducing a nucleotide sequence in a plant in a manner to cause stable or transient expression of the sequence.

Successful examples of the modification of plant characteristics by transformation with cloned sequences which serve to illustrate the current knowledge in this field of technology, and which are herein incorporated by reference, include: U.S. Patent Nos.
20 5,571,706; 5,677,175; 5,510,471; 5,750,386; 5,597,945; 5,589,615; 5,750,871; 5,268,526; 5,780,708; 5,538,880; 5,773,269; 5,736,369 and 5,610,042.

Following transformation, plants are preferably selected using a dominant selectable marker incorporated into the transformation vector. Typically, such a marker will confer antibiotic or herbicide resistance on the transformed plants, and selection of transformants
25 can be accomplished by exposing the plants to appropriate concentrations of the antibiotic or herbicide.

After transformed plants are selected and grown to maturity, those plants showing a modified trait are identified. The modified trait can be any of those traits described above. Additionally, to confirm that the modified trait is due to changes in expression levels or
30 activity of the polypeptide or polynucleotide of the invention can be determined by analyzing mRNA expression using Northern blots, RT-PCR or microarrays, or protein expression using immunoblots or Western blots or gel shift assays.

INTEGRATED SYSTEMS—SEQUENCE IDENTITY

Additionally, the present invention may be an integrated system, computer or computer readable medium that comprises an instruction set for determining the identity of one or more sequences in a database. In addition, the instruction set can be used to generate or identify sequences that meet any specified criteria. Furthermore, the instruction set may be used to associate or link certain functional benefits, such improved environmental stress tolerance, with one or more identified sequence.

For example, the instruction set can include, e.g., a sequence comparison or other alignment program, e.g., an available program such as, for example, the Wisconsin Package Version 10.0, such as BLAST, FASTA, PILEUP, FINDPATTERNS or the like (GCG, Madison, WI). Public sequence databases such as GenBank, EMBL, Swiss-Prot and PIR or private sequence databases such as PhytoSeq (Incyte Pharmaceuticals, Palo Alto, CA) can be searched.

Alignment of sequences for comparison can be conducted by the local homology algorithm of Smith and Waterman (1981) Adv. Appl. Math. 2:482, by the homology alignment algorithm of Needleman and Wunsch (1970) J. Mol. Biol. 48:443, by the search for similarity method of Pearson and Lipman (1988) Proc. Natl. Acad. Sci. U.S.A. 85: 2444, by computerized implementations of these algorithms. After alignment, sequence comparisons between two (or more) polynucleotides or polypeptides are typically performed by comparing sequences of the two sequences over a comparison window to identify and compare local regions of sequence similarity. The comparison window can be a segment of at least about 20 contiguous positions, usually about 50 to about 200, more usually about 100 to about 150 contiguous positions. A description of the method is provided in Ausubel et al., *supra*.

A variety of methods of determining sequence relationships can be used, including manual alignment and computer assisted sequence alignment and analysis. This later approach is a preferred approach in the present invention, due to the increased throughput afforded by computer assisted methods. As noted above, a variety of computer programs for performing sequence alignment are available, or can be produced by one of skill.

One example algorithm that is suitable for determining percent sequence identity and sequence similarity is the BLAST algorithm, which is described in Altschul et al. J. Mol. Biol. 215:403-410 (1990). Software for performing BLAST analyses is publicly available, e.g., through the National Center for Biotechnology Information (<http://www.ncbi.nlm.nih.gov/>). This algorithm involves first identifying high scoring sequence pairs (HSPs) by identifying short words of length W in the query sequence, which either match or satisfy some positive-valued threshold score T when aligned with a word of the same length in a database sequence. T is

referred to as the neighborhood word score threshold (Altschul et al., *supra*). These initial neighborhood word hits act as seeds for initiating searches to find longer HSPs containing them. The word hits are then extended in both directions along each sequence for as far as the cumulative alignment score can be increased. Cumulative scores are calculated using, for nucleotide sequences, the parameters M (reward score for a pair of matching residues; always > 0) and N (penalty score for mismatching residues; always < 0). For amino acid sequences, a scoring matrix is used to calculate the cumulative score. Extension of the word hits in each direction are halted when: the cumulative alignment score falls off by the quantity X from its maximum achieved value; the cumulative score goes to zero or below, due to the accumulation of one or more negative-scoring residue alignments; or the end of either sequence is reached. The BLAST algorithm parameters W, T, and X determine the sensitivity and speed of the alignment. The BLASTN program (for nucleotide sequences) uses as defaults a wordlength (W) of 11, an expectation (E) of 10, a cutoff of 100, M=5, N=-4, and a comparison of both strands. For amino acid sequences, the BLASTP program uses as defaults a wordlength (W) of 3, an expectation (E) of 10, and the BLOSUM62 scoring matrix (*see* Henikoff & Henikoff (1989) Proc. Natl. Acad. Sci. USA 89:10915).

In addition to calculating percent sequence identity, the BLAST algorithm also performs a statistical analysis of the similarity between two sequences (*see*, e.g., Karlin & Altschul (1993) Proc. Natl. Acad. Sci. USA 90:5873-5787). One measure of similarity provided by the BLAST algorithm is the smallest sum probability (P(N)), which provides an indication of the probability by which a match between two nucleotide or amino acid sequences would occur by chance. For example, a nucleic acid is considered similar to a reference sequence (and, therefore, in this context, homologous) if the smallest sum probability in a comparison of the test nucleic acid to the reference nucleic acid is less than about 0.1, or less than about 0.01, and or even less than about 0.001. An additional example of a useful sequence alignment algorithm is PILEUP. PILEUP creates a multiple sequence alignment from a group of related sequences using progressive, pairwise alignments. The program can align, e.g., up to 300 sequences of a maximum length of 5,000 letters.

The integrated system, or computer typically includes a user input interface allowing a user to selectively view one or more sequence records corresponding to the one or more character strings, as well as an instruction set which aligns the one or more character strings with each other or with an additional character string to identify one or more region of sequence similarity. The system may include a link of one or more character strings with a particular

phenotype or gene function. Typically, the system includes a user readable output element which displays an alignment produced by the alignment instruction set.

The methods of this invention can be implemented in a localized or distributed computing environment. In a distributed environment, the methods may implemented on a single computer comprising multiple processors or on a multiplicity of computers. The computers can be linked, e.g. through a common bus, but more preferably the computer(s) are nodes on a network. The network can be a generalized or a dedicated local or wide-area network and, in certain preferred embodiments, the computers may be components of an intra-net or an internet.

Thus, the invention provides methods for identifying a sequence similar or homologous to one or more polynucleotides as noted herein, or one or more target polypeptides encoded by the polynucleotides, or otherwise noted herein and may include linking or associating a given plant phenotype or gene function with a sequence. In the methods, a sequence database is provided (locally or across an inter or intra net) and a query is made against the sequence database using the relevant sequences herein and associated plant phenotypes or gene functions.

Any sequence herein can be entered into the database, before or after querying the database. This provides for both expansion of the database and, if done before the querying step, for insertion of control sequences into the database. The control sequences can be detected by the query to ensure the general integrity of both the database and the query. As noted, the query can be performed using a web browser based interface. For example, the database can be a centralized public database such as those noted herein, and the querying can be done from a remote terminal or computer across an internet or intranet.

EXAMPLES

The following examples are intended to illustrate but not limit the present invention.

25 EXAMPLE I. FULL LENGTH GENE IDENTIFICATION AND CLONING

Putative transcription factor sequences (genomic or ESTs) related to known transcription factors were identified in the *Arabidopsis thaliana* GenBank database using the tblastn sequence analysis program using default parameters and a P-value cutoff threshold of -4 or -5 or lower, depending on the length of the query sequence. Putative transcription factor sequence hits were then screened to identify those containing particular sequence strings. If the sequence hits contained such sequence strings, the sequences were confirmed as transcription factors.

Alternatively, *Arabidopsis thaliana* cDNA libraries derived from different tissues or treatments, or genomic libraries were screened to identify novel members of a transcription family using a low stringency hybridization approach. Probes were synthesized using gene specific primers in a standard PCR reaction (annealing temperature 60° C) and labeled with ³²P dCTP using the High Prime DNA Labeling Kit (Boehringer Mannheim). Purified radiolabelled probes were added to filters immersed in Church hybridization medium (0.5 M NaPO₄ pH 7.0, 7% SDS, 1 % w/v bovine serum albumin) and hybridized overnight at 60 °C with shaking. Filters were washed two times for 45 to 60 minutes with 1xSSC, 1% SDS at 60° C.

To identify additional sequence 5' or 3' of a partial cDNA sequence in a cDNA library, 5' and 3' rapid amplification of cDNA ends (RACE) was performed using the Marathon™ cDNA amplification kit (Clontech, Palo Alto, CA). Generally, the method entailed first isolating poly(A) mRNA, performing first and second strand cDNA synthesis to generate double stranded cDNA, blunting cDNA ends, followed by ligation of the Marathon™ Adaptor to the cDNA to form a library of adaptor-ligated ds cDNA.

Gene-specific primers were designed to be used along with adaptor specific primers for both 5' and 3' RACE reactions. Nested primers, rather than single primers, were used to increase PCR specificity. Using 5' and 3' RACE reactions, 5' and 3' RACE fragments were obtained, sequenced and cloned. The process can be repeated until 5' and 3' ends of the full-length gene were identified. Then the full-length cDNA was generated by PCR using primers specific to 5' and 3' ends of the gene by end-to-end PCR.

EXAMPLE II. CONSTRUCTION OF EXPRESSION VECTORS

The sequence was amplified from a genomic or cDNA library using primers specific to sequences upstream and downstream of the coding region. The expression vector was pMEN20 or pMEN65, which are both derived from pMON316 (Sanders et al, (1987) Nucleic Acids Research 15:1543-58) and contain the CaMV 35S promoter to express transgenes. To clone the sequence into the vector, both pMEN20 and the amplified DNA fragment were digested separately with SalI and NotI restriction enzymes at 37° C for 2 hours. The digestion products were subject to electrophoresis in a 0.8% agarose gel and visualized by ethidium bromide staining. The DNA fragments containing the sequence and the linearized plasmid were excised and purified by using a Qiaquick gel extraction kit (Qiagen, CA). The fragments of interest were ligated at a ratio of 3:1 (vector to insert). Ligation reactions using T4 DNA ligase (New England Biolabs, MA) were carried out at 16° C for 16 hours. The ligated DNAs were transformed into

competent cells of the *E. coli* strain DH5alpha by using the heat shock method. The transformations were plated on LB plates containing 50 mg/l kanamycin (Sigma).

Individual colonies were grown overnight in five milliliters of LB broth containing 50 mg/l kanamycin at 37° C. Plasmid DNA was purified by using Qiaquick Mini
5 Prep kits (Qiagen, CA).

EXAMPLE III. TRANSFORMATION OF *AGROBACTERIUM* WITH THE EXPRESSION VECTOR

After the plasmid vector containing the gene was constructed, the vector was used to transform *Agrobacterium tumefaciens* cells expressing the gene products. The stock of
10 *Agrobacterium tumefaciens* cells for transformation were made as described by Nagel et al. (1990) FEMS Microbiol Letts. 67: 325-328. *Agrobacterium* strain ABI was grown in 250 ml LB medium (Sigma) overnight at 28°C with shaking until an absorbance (A_{600}) of 0.5 – 1.0 was reached. Cells were harvested by centrifugation at 4,000 x g for 15 min at 4° C. Cells were then resuspended in 250 µl chilled buffer (1 mM HEPES, pH adjusted to 7.0 with KOH). Cells were
15 centrifuged again as described above and resuspended in 125 µl chilled buffer. Cells were then centrifuged and resuspended two more times in the same HEPES buffer as described above at a volume of 100 µl and 750 µl, respectively. Resuspended cells were then distributed into 40 µl aliquots, quickly frozen in liquid nitrogen, and stored at -80° C.

Agrobacterium cells were transformed with plasmids prepared as described
20 above following the protocol described by Nagel et al. For each DNA construct to be transformed, 50 – 100 ng DNA (generally resuspended in 10 mM Tris-HCl, 1 mM EDTA, pH 8.0) was mixed with 40 µl of *Agrobacterium* cells. The DNA/cell mixture was then transferred to a chilled cuvette with a 2mm electrode gap and subject to a 2.5 kV charge dissipated at 25 µF and 200 µF using a Gene Pulser II apparatus (Bio-Rad). After electroporation, cells were
25 immediately resuspended in 1.0 ml LB and allowed to recover without antibiotic selection for 2 – 4 hours at 28° C in a shaking incubator. After recovery, cells were plated onto selective medium of LB broth containing 100 µg/ml spectinomycin (Sigma) and incubated for 24-48 hours at 28° C. Single colonies were then picked and inoculated in fresh medium. The presence of the plasmid construct was verified by PCR amplification and sequence analysis.

EXAMPLE IV. TRANSFORMATION OF *ARABIDOPSIS* PLANTS WITH *AGROBACTERIUM TUMEFACIENS* WITH EXPRESSION VECTOR

After transformation of *Agrobacterium tumefaciens* with plasmid vectors containing the gene, single *Agrobacterium* colonies were identified, propagated, and used to

transform *Arabidopsis* plants. Briefly, 500 ml cultures of LB medium containing 50 mg/l kanamycin were inoculated with the colonies and grown at 28° C with shaking for 2 days until an absorbance (A_{600}) of > 2.0 is reached. Cells were then harvested by centrifugation at 4,000 x g for 10 min, and resuspended in infiltration medium (1/2 X Murashige and Skoog salts (Sigma), 1 X Gamborg's B-5 vitamins (Sigma), 5.0% (w/v) sucrose (Sigma), 0.044 μ M benzylamino purine (Sigma), 200 μ L/L Silwet L-77 (Lehle Seeds) until an absorbance (A_{600}) of 0.8 was reached.

Prior to transformation, *Arabidopsis thaliana* seeds (ecotype Columbia) were sown at a density of ~10 plants per 4" pot onto Pro-Mix BX potting medium (Hummert International) covered with fiberglass mesh (18 mm X 16 mm). Plants were grown under continuous illumination (50-75 μ E/m²/sec) at 22-23° C with 65-70% relative humidity. After about 4 weeks, primary inflorescence stems (bolts) are cut off to encourage growth of multiple secondary bolts. After flowering of the mature secondary bolts, plants were prepared for transformation by removal of all siliques and opened flowers.

The pots were then immersed upside down in the mixture of *Agrobacterium* infiltration medium as described above for 30 sec, and placed on their sides to allow draining into a 1' x 2' flat surface covered with plastic wrap. After 24 h, the plastic wrap was removed and pots are turned upright. The immersion procedure was repeated one week later, for a total of two immersions per pot. Seeds were then collected from each transformation pot and analyzed following the protocol described below.

EXAMPLE V. IDENTIFICATION OF ARABIDOPSIS PRIMARY TRANSFORMANTS

Seeds collected from the transformation pots were sterilized essentially as follows. Seeds were dispersed into in a solution containing 0.1% (v/v) Triton X-100 (Sigma) and sterile H₂O and washed by shaking the suspension for 20 min. The wash solution was then drained and replaced with fresh wash solution to wash the seeds for 20 min with shaking. After removal of the second wash solution, a solution containing 0.1% (v/v) Triton X-100 and 70% ethanol (Equistar) was added to the seeds and the suspension was shaken for 5 min. After removal of the ethanol/detergent solution, a solution containing 0.1% (v/v) Triton X-100 and 30% (v/v) bleach (Clorox) was added to the seeds, and the suspension was shaken for 10 min. After removal of the bleach/detergent solution, seeds were then washed five times in sterile distilled H₂O. The seeds were stored in the last wash water at 4° C for 2 days in the dark before being plated onto antibiotic selection medium (1 X Murashige and Skoog salts (pH adjusted to 5.7 with 1M KOH), 1 X Gamborg's B-5 vitamins, 0.9% phytagar (Life Technologies), and 50 mg/l kanamycin). Seeds were germinated under continuous illumination (50-75 μ E/m²/sec) at 22-23°

C. After 7-10 days of growth under these conditions, kanamycin resistant primary transformants (T₁ generation) were visible and obtained. These seedlings were transferred first to fresh selection plates where the seedlings continued to grow for 3-5 more days, and then to soil (Pro-Mix BX potting medium).

Primary transformants were crossed and progeny seeds (T₂) collected; kanamycin resistant seedlings were selected and analyzed. The expression levels of the recombinant polynucleotides in the transformants varies from about a 5% expression level increase to a least a 100% expression level increase. Similar observations are made with respect to polypeptide level expression.

EXAMPLE VI. IDENTIFICATION OF ARABIDOPSIS PLANTS WITH TRANSCRIPTION FACTOR GENE KNOCKOUTS

The screening of insertion mutagenized *Arabidopsis* collections for null mutants in a known target gene was essentially as described in Krysan et al (1999) Plant Cell 11:2283-2290. Briefly, gene-specific primers, nested by 5-250 base pairs to each other, were designed from the 5' and 3' regions of a known target gene. Similarly, nested sets of primers were also created specific to each of the T-DNA or transposon ends (the "right" and "left" borders). All possible combinations of gene specific and T-DNA/transposon primers were used to detect by PCR an insertion event within or close to the target gene. The amplified DNA fragments were then sequenced which allows the precise determination of the T-DNA/transposon insertion point relative to the target gene. Insertion events within the coding or intervening sequence of the genes were deconvoluted from a pool comprising a plurality of insertion events to a single unique mutant plant for functional characterization. The method is described in more detail in Yu and Adam, US Application Serial No. 09/177,733 filed October 23, 1998.

EXAMPLE VII. IDENTIFICATION OF ENVIRONMENTAL STRESS TOLERANCE PHENOTYPE IN OVEREXPRESSOR OR GENE KNOCKOUT PLANTS

Experiments were performed to identify those transformants or knockouts that exhibited an improved environmental stress tolerance. For such studies, the transformants were exposed to a variety of environmental stresses. Plants were exposed to chilling stress (6 hour exposure to 4-8°C), heat stress (6 hour exposure to 32-37°C), high salt stress (6 hour exposure to 200 mM NaCl), drought stress (168 hours after removing water from trays), osmotic stress (6 hour exposure to 3 M mannitol), or nutrient limitation (nitrogen, phosphate, and potassium) (Nitrogen: all components of MS medium remained constant except N was reduced to 20mg/L of

NH₄NO₃, or Phosphate: All components of MS medium except KH₂PO₄, which was replaced by K₂SO₄, Potassium: All components of MS medium except removal of KNO₃ and KH₂PO₄, which were replaced by NaH₄PO₄).

5 Table 3 shows the phenotypes observed for particular overexpressor or knockout plants and provides the SEQ ID No., the internal reference code (GID), whether a knockout or overexpressor plant was analyzed and the observed phenotype.

Table 3

SEQ ID No.	GID	Knockout (KO) or overexpressor (OX)	Phenotype observed
1	G22	OE	Increased tolerance to high salt
3	G188	KO	Better germination under osmotic stress
5	G225	OE	Increased tolerance to nitrogen-limited medium
7	G226	OE	Increased tolerance to nitrogen-limited medium
9	G256	OE	Better germination and growth in cold
11	G419	OE	Increased tolerance to potassium-free medium
13	G464	OE	Better germination and growth in heat
15	G482	OE	Increased tolerance to high salt
17	G502	KO	Increased sensitivity to osmotic stress
19	G526	OE	Increased sensitivity to osmotic stress
21	G545	OE	Susceptible to high salt
23	G561	OE	Increased tolerance to potassium-free medium
25	G664	OE	Better germination and growth in cold
27	G682	OE	Better germination and growth in heat
29	G911	OE	Increased growth on potassium-free medium
31	G964	OE	Better germination and growth in heat
33	G394	OE	More sensitive to chilling
35	G489	OE	Increased tolerance to osmotic stress

10 For a particular overexpressor that shows a decreased tolerance to an environmental stress, it may be more useful to select a plant with a decreased expression of the particular transcription factor. For a particular knockout that shows a decreased tolerance to an environmental stress, it may be more useful to select a plant with an increased expression of the particular transcription factor.

EXAMPLE VIII. IDENTIFICATION OF HOMOLOGOUS SEQUENCES

15 Homologous sequences from *Arabidopsis* and plant species other than *Arabidopsis* were identified using database sequence search tools, such as the Basic Local Alignment Search Tool (BLAST) (Altschul et al. (1990) *J. Mol. Biol.* 215:403-410; and Altschul et al. (1997) *Nucl. Acid Res.* 25: 3389-3402). The tblastx sequence analysis programs were employed using the

BLOSUM-62 scoring matrix (Henikoff, S. and Henikoff, J. G. (1992) Proc. Natl. Acad. Sci. USA 89: 10915-10919).

Identified *Arabidopsis* homologous sequences are provided in Figure 2 and included in the Sequence Listing. The percent sequence identity among these sequences is as low as 47% sequence identity. Additionally, the entire NCBI GenBank database was filtered for sequences from all plants except *Arabidopsis thaliana* by selecting all entries in the NCBI GenBank database associated with NCBI taxonomic ID 33090 (Viridiplantae; all plants) and excluding entries associated with taxonomic ID 3701 (*Arabidopsis thaliana*). These sequences were compared to sequences representing genes of SEQ IDs Nos. 1-54 on 9/26/2000 using the Washington University TBLASTX algorithm (version 2.0a19MP). For each gene of SEQ IDs Nos. 1-54, individual comparisons were ordered by probability score (P-value), where the score reflects the probability that a particular alignment occurred by chance. For example, a score of $3.6e-40$ is 3.6×10^{-40} . For up to ten species, the gene with the lowest P-value (and therefore the most likely homolog) is listed in Figure 3.

In addition to P-values, comparisons were also scored by percentage identity. Percentage identity reflects the degree to which two segments of DNA or protein are identical over a particular length. The ranges of percent identity between the non-*Arabidopsis* genes shown in Figure 3 and the *Arabidopsis* genes in the sequence listing are: SEQ ID No. 1: 53%-67%; SEQ ID No. 3: 38%-76%; SEQ ID No. 5: 34%-67%; SEQ ID No. 7: 50%-69%; SEQ ID No. 9: 32%-91%; SEQ ID No. 11: 48%-66%; SEQ ID No. 13: 34%-60%; SEQ ID No. 15: 58%-81%; SEQ ID No. 17: 65%-94%; SEQ ID No. 19: 72%-83%; SEQ ID No. 21: 52%-64%; SEQ ID No. 23: 40%-89%; SEQ ID No. 25: 86%-97%; SEQ ID No. 27: 41%-75%; SEQ ID No. 29: 29%-72%; SEQ ID No. 31: 49%-70%; SEQ ID No. 33: 56%-86%; SEQ ID No. 35: 61%-84%; SEQ ID No. 37: 40%-58%; SEQ ID No. 39: 63%-87%; SEQ ID No. 41: 51%-88%; SEQ ID No. 43: 80%-90%; SEQ ID No. 45: 79%-90%; SEQ ID No. 47: 30%-58%; SEQ ID No. 49: 52%-62%; SEQ ID No. 51: 55%-73% and SEQ ID No. 53: 44%-80%.

The polynucleotides and polypeptides in the Sequence Listing and the identified homologous sequences may be stored in a computer system and have associated or linked with the sequences a function, such as that the polynucleotides and polypeptides are useful for modifying the environmental stress tolerance of a plant.

All references, publications, patents and other documents herein are incorporated by reference in their entirety for all purposes. Although the invention has been described with

reference to the embodiments and examples above, it should be understood that various modifications can be made without departing from the spirit of the invention.

What is claimed is:

1. A transgenic plant with modified environmental stress tolerance, which plant comprises a recombinant polynucleotide comprising a nucleotide sequence selected from the group consisting of:

- 5 (a) a nucleotide sequence encoding a polypeptide comprising a sequence selected from SEQ ID Nos. 2N, where N=1-27, or a complementary nucleotide sequence thereof;
- (b) a nucleotide sequence encoding a polypeptide comprising a conservatively substituted variant of a polypeptide of (a);
- 10 (c) a nucleotide sequence comprising a sequence selected from those of SEQ ID Nos. 2N-1, where N=1-27, or a complementary nucleotide sequence thereof;
- (d) a nucleotide sequence comprising silent substitutions in a nucleotide sequence of (c);
- (e) a nucleotide sequence which hybridizes under stringent conditions to a nucleotide sequence of one or more of: (a), (b), (c), or (d);
- 15 (f) a nucleotide sequence comprising at least 15 consecutive nucleotides of a sequence of any of (a)-(e);
- (g) a nucleotide sequence comprising a subsequence or fragment of any of (a)-(f), which subsequence or fragment encodes a polypeptide that modifies a plant's environmental stress tolerance;
- (h) a nucleotide sequence having at least 30% sequence identity to a nucleotide sequence of any of (a)-(g);
- 20 (i) a nucleotide sequence having at least 60% identity sequence identity to a nucleotide sequence of any of (a)-(g);
- (j) a nucleotide sequence which encodes a polypeptide having at least 30% identity sequence identity to a polypeptide of SEQ ID Nos. 2N, where N=1-27;
- 25 (k) a nucleotide sequence which encodes a polypeptide having at least 60% identity sequence identity to a polypeptide of SEQ ID Nos. 2N, where N=1-27; and
- (l) a nucleotide sequence which encodes a polypeptide having at least 65% sequence identity to a conserved domain of a polypeptide of SEQ ID Nos. 2N, where N=1-27.

30 2. The transgenic plant of claim 1, further comprising a constitutive, inducible, or tissue-active promoter operably linked to said nucleotide sequence.

3. The transgenic plant of claim 1, wherein the plant is selected from the group consisting of: soybean, wheat, corn, potato, cotton, rice, oilseed rape, sunflower, alfalfa, sugarcane, turf,

banana, blackberry, blueberry, strawberry, raspberry, cantaloupe, carrot, cauliflower, coffee, cucumber, eggplant, grapes, honeydew, lettuce, mango, melon, onion, papaya, peas, peppers, pineapple, spinach, squash, sweet corn, tobacco, tomato, watermelon, rosaceous fruits, and vegetable brassicas.

5

4. An isolated or recombinant polynucleotide comprising a nucleotide sequence selected from the group consisting of:

(a) a nucleotide sequence encoding a polypeptide comprising a sequence selected from SEQ ID Nos. 2N, where N=1-27, or a complementary nucleotide sequence thereof;

10

(b) a nucleotide sequence encoding a polypeptide comprising a conservatively substituted variant of a polypeptide of (a);

(c) a nucleotide sequence comprising a sequence selected from those of SEQ ID Nos. 2N-1, where N=1-27, or a complementary nucleotide sequence thereof;

(d) a nucleotide sequence comprising silent substitutions in a nucleotide sequence of (c);

15

(e) a nucleotide sequence which hybridizes under stringent conditions to a nucleotide sequence of one or more of: (a), (b), (c), or (d);

(f) a nucleotide sequence comprising at least 15 consecutive nucleotides of a sequence of any of (a)-(e);

20

(g) a nucleotide sequence comprising a subsequence or fragment of any of (a)-(f), which subsequence or fragment encodes a polypeptide that modifies a plant's environmental stress tolerance;

(h) a nucleotide sequence having at least 30% sequence identity to a nucleotide sequence of any of (a)-(g);

25

(i) a nucleotide sequence having at least 60% identity sequence identity to a nucleotide sequence of any of (a)-(g);

(j) a nucleotide sequence which encodes a polypeptide having at least 30% identity sequence identity to a polypeptide of SEQ ID Nos. 2N, where N=1-27;

(k) a nucleotide sequence which encodes a polypeptide having at least 60% identity sequence identity to a polypeptide of SEQ ID Nos. 2N, where N=1-27; and

30

(l) a nucleotide sequence which encodes a conserved domain of a polypeptide having at least 65% sequence identity to a conserved domain of a polypeptide of SEQ ID Nos. 2N, where N=1-27.

5. The isolated or recombinant polynucleotide of claim 4, further comprising a constitutive, inducible, or tissue-active promoter operably linked to the nucleotide sequence.

6. A cloning or expression vector comprising the isolated or recombinant polynucleotide of claim 4.

7. A cell comprising the cloning or expression vector of claim 6.

8. A transgenic plant comprising the isolated or recombinant polynucleotide of claim 4.

9. A composition produced by one or more of:

(a) incubating one or more polynucleotide of claim 4 with a nuclease;

(b) incubating one or more polynucleotide of claim 4 with a restriction enzyme;

(c) incubating one or more polynucleotide of claim 4 with a polymerase;

(d) incubating one or more polynucleotide of claim 4 with a polymerase and a primer;

(e) incubating one or more polynucleotide of claim 4 with a cloning vector, or

(f) incubating one or more polynucleotide of claim 4 with a cell.

10. A composition comprising two or more different polynucleotides of claim 4.

11. An isolated or recombinant polypeptide comprising a subsequence of at least about 15 contiguous amino acids encoded by the recombinant or isolated polynucleotide of claim 4.

12. A plant ectopically expressing an isolated polypeptide of claim 11.

13. A method for producing a plant having a modified environmental stress tolerance, the method comprising altering the expression of the isolated or recombinant polynucleotide of claim 4 or the expression levels or activity of a polypeptide of claim 11 in a plant, thereby producing a modified plant, and selecting the modified plant for improved environmental stress tolerance thereby providing the modified plant with a modified environmental stress tolerance.

14. The method of claim 13, wherein the polynucleotide is a polynucleotide of claim 4.

15. A method of identifying a factor that is modulated by or interacts with a polypeptide encoded by a polynucleotide of claim 4, the method comprising:

- (a) expressing a polypeptide encoded by the polynucleotide in a plant; and
- (b) identifying at least one factor that is modulated by or interacts with the polypeptide.

5

16. The method of claim 15, wherein the identifying is performed by detecting binding by the polypeptide to a promoter sequence, or detecting interactions between an additional protein and the polypeptide in a yeast two hybrid system.

10 17. The method of claim 15, wherein the identifying is performed by detecting expression of a factor by hybridization to a microarray, subtractive hybridization or differential display.

18. A method of identifying a molecule that modulates activity or expression of a polynucleotide or polypeptide of interest, the method comprising:

- 15 (a) placing the molecule in contact with a plant comprising the polynucleotide or polypeptide encoded by the polynucleotide of claim 4; and
- (b) monitoring one or more of:
 - (i) expression level of the polynucleotide in the plant;
 - (ii) expression level of the polypeptide in the plant;
 - 20 (iii) modulation of an activity of the polypeptide in the plant; or
 - (iv) modulation of an activity of the polynucleotide in the plant.

19. An integrated system, computer or computer readable medium comprising one or more character strings corresponding to a polynucleotide of claim 4, or to a polypeptide encoded by the polynucleotide.

25

20. The integrated system, computer or computer readable medium of claim 19, further comprising a link between said one or more sequence strings to a modified plant environmental stress tolerance phenotype.

30

21. A method of identifying a sequence similar or homologous to one or more polynucleotides of claim 4, or one or more polypeptides encoded by the polynucleotides, the method comprising:

- (a) providing a sequence database; and,

(b) querying the sequence database with one or more target sequences corresponding to the one or more polynucleotides or to the one or more polypeptides to identify one or more sequence members of the database that display sequence similarity or homology to one or more of the one or more target sequences.

5

22. The method of claim 21, wherein the querying comprises aligning one or more of the target sequences with one or more of the one or more sequence members in the sequence database.

10

23. The method of claim 21, wherein the querying comprises identifying one or more of the one or more sequence members of the database that meet a user-selected identity criteria with one or more of the target sequences.

15

24. The method of claim 21, further comprising linking the one or more of the polynucleotides of claim 4, or encoded polypeptides, to a modified plant environmental stress tolerance phenotype.

20

25. A plant comprising altered expression levels of an isolated or recombinant polynucleotide of claim 4.

26. A plant comprising altered expression levels or the activity of an isolated or recombinant polypeptide of claim 11.

25

27. A plant lacking a nucleotide sequence encoding a polypeptide of claim 11.

Figure 1

SEQ ID No.	GID	cDNA or protein	conserved domain
1	G22	cDNA	
2	G22	protein	89-157
3	G188	cDNA	
4	G188	protein	175-222
5	G225	cDNA	
6	G225	protein	39-76
7	G226	cDNA	
8	G226	protein	28-78
9	G256	cDNA	
10	G256	protein	13-115
11	G419	cDNA	
12	G419	protein	392-452
13	G464	cDNA	
14	G464	protein	7-15,70-80,125-158,183-219
15	G482	cDNA	
16	G482	protein	25-116
17	G502	cDNA	
18	G502	protein	10-155
19	G526	cDNA	
20	G526	protein	21-149
21	G545	cDNA	
22	G545	protein	82-102, 136-154
23	G561	cDNA	
24	G561	protein	248-308
25	G664	cDNA	
26	G664	protein	13-116
27	G682	cDNA	
28	G682	protein	22-53
29	G911	cDNA	
30	G911	protein	86-129
31	G964	cDNA	
32	G964	protein	126-186
33	G394	cDNA	
34	G394	protein	121-182
35	G489	cDNA	
36	G489	protein	57-156

Figure 2

SEQ ID No.	GID	homolog	cDNA or protein	conserved domain
37	G463	homolog of G464	cDNA	
38	G463	homolog of G464	protein	14-23, 77-88, 130-146, 194-227
39	G767	homolog of G502	cDNA	
40	G767	homolog of G502	protein	8-158
41	G765	homolog of G526	cDNA	
42	G765	homolog of G526	protein	23-167
43	G197	homolog of G664	cDNA	
44	G197	homolog of G664	protein	14-119
45	G255	homolog of G664	cDNA	
46	G255	homolog of G664	protein	14-115
47	G1113	homolog of G911	cDNA	
48	G1113	homolog of G911	protein	85-128
49	G398	homolog of G964	cDNA	
50	G398	homolog of G964	protein	128-191
51	G395	homolog of G394	cDNA	
52	G395	homolog of G394	protein	72-135
53	G393	homolog of G394	cDNA	
54	G393	homolog of G394	protein	106-169

Figure 3A

SEQ ID No.	GID	Genbank NID	P-value	Species
1	G22	790359	1.00E-45	Nicotiana tabacum
1	G22	3342210	6.60E-45	Lycopersicon esculentum
1	G22	6654776	1.60E-44	Medicago truncatula
1	G22	8809570	5.80E-44	Nicotiana glauca
1	G22	7627061	2.40E-39	Gossypium arboreum
1	G22	7324479	9.50E-36	Lycopersicon pennellii
1	G22	8980312	4.30E-31	Catharanthus roseus
1	G22	7528275	1.20E-30	Mesembryanthemum crystallinum
1	G22	6478844	4.60E-28	Matricaria chamomilla
1	G22	6847348	5.90E-26	Glycine max
3	G188	7779802	5.20E-36	Lotus japonicus
3	G188	7284340	2.10E-34	Glycine max
3	G188	9361307	1.20E-27	Triticum aestivum
3	G188	7340336	1.10E-22	Oryza sativa
3	G188	6529152	3.60E-22	Lycopersicon esculentum
3	G188	8748477	7.70E-21	Medicago truncatula
3	G188	5456433	7.10E-14	Zea mays
3	G188	9302479	1.60E-12	Sorghum bicolor
3	G188	6696287	4.10E-12	Pinus taeda
3	G188	562242	9.00E-12	Brassica rapa
5	G225	4396287	4.40E-16	Glycine max
5	G225	309571	0.00029	Zea mays
5	G225	3857004	0.001	Populus tremula x Populus tremuloides
5	G225	9410205	0.019	Triticum aestivum
5	G225	9426190	0.025	Triticum turgidum subsp. durum
5	G225	8382118	0.046	Gossypium arboreum
5	G225	6782756	0.27	Oryza sativa
5	G225	7721017	0.4	Lotus japonicus
5	G225	6020136	0.47	Pinus taeda
5	G225	2921331	0.48	Gossypium hirsutum
7	G226	4396287	5.10E-15	Glycine max
7	G226	9410205	1.50E-05	Triticum aestivum
7	G226	3857004	0.11	Populus tremula x Populus tremuloides
7	G226	2428139	0.35	Oryza sativa
9	G256	1430847	1.30E-72	Lycopersicon esculentum
9	G256	9252441	1.20E-65	Solanum tuberosum
9	G256	8380712	2.20E-58	Gossypium arboreum
9	G256	8172976	1.60E-54	Medicago truncatula
9	G256	9205295	1.30E-44	Glycine max
9	G256	20562	6.40E-40	Petunia x hybrida
9	G256	4886263	4.40E-37	Antirrhinum majus
9	G256	6552360	5.00E-36	Nicotiana tabacum
9	G256	2312003	1.20E-35	Oryza sativa
9	G256	5268628	5.20E-35	Zea mays
11	G419	7239156	2.60E-59	Malus x domestica
11	G419	5278451	9.00E-58	Lycopersicon esculentum
11	G419	9205496	1.30E-55	Glycine max
11	G419	7628137	9.30E-51	Gossypium arboreum
11	G419	6069643	9.50E-51	Oryza sativa
11	G419	7562931	9.80E-45	Medicago truncatula
11	G419	7322293	2.30E-37	Lycopersicon hirsutum
11	G419	8404716	1.10E-29	Hordeum vulgare
11	G419	7217755	1.40E-29	Sorghum bicolor

Figure 3B

SEQ ID No.	GID	Genbank NID	P-value	Species
11	G419	9428023	4.60E-28	Triticum aestivum
13	G464	6527230	3.60E-31	Lycopersicon esculentum
13	G464	9305572	1.10E-22	Sorghum bicolor
13	G464	6604917	6.70E-22	Medicago truncatula
13	G464	5058123	2.30E-21	Glycine max
13	G464	3760881	1.20E-19	Oryza sativa
13	G464	5044476	1.20E-17	Gossypium hirsutum
13	G464	9412603	6.40E-15	Triticum aestivum
13	G464	7777277	3.20E-13	Lotus japonicus
13	G464	9410371	1.70E-11	Hordeum vulgare
13	G464	7624108	2.10E-10	Gossypium arboreum
15	G482	7691987	5.50E-50	Glycine max
15	G482	7781090	1.30E-48	Lotus japonicus
15	G482	7409616	1.10E-47	Lycopersicon esculentum
15	G482	9416562	4.40E-46	Triticum aestivum
15	G482	22379	2.30E-44	Zea mays
15	G482	7501372	7.70E-44	Gossypium arboreum
15	G482	7765436	8.40E-42	Medicago truncatula
15	G482	5044464	1.20E-40	Gossypium hirsutum
15	G482	9441376	9.20E-40	Chlamydomonas reinhardtii
15	G482	8071558	3.50E-39	Solanum tuberosum
17	G502	6730941	1.60E-91	Oryza sativa
17	G502	7765679	1.60E-82	Medicago truncatula
17	G502	7502501	7.30E-80	Gossypium arboreum
17	G502	5510359	8.30E-77	Glycine max
17	G502	5601137	8.70E-76	Lycopersicon esculentum
17	G502	9302206	1.40E-73	Sorghum bicolor
17	G502	4089948	3.40E-50	Brassica napus
17	G502	8329134	7.90E-49	Mesembryanthemum crystallinum
17	G502	7723564	8.60E-49	Lotus japonicus
17	G502	4218534	1.80E-48	Triticum sp.
19	G526	5049217	3.40E-61	Gossypium hirsutum
19	G526	6066594	1.50E-55	Petunia x hybrida
19	G526	4384535	1.50E-54	Lycopersicon esculentum
19	G526	6454868	6.60E-54	Glycine max
19	G526	4977542	4.70E-52	Oryza sativa
19	G526	5343151	7.00E-51	Zea mays
19	G526	9361647	5.10E-50	Triticum aestivum
19	G526	6799764	4.30E-48	Medicago truncatula
19	G526	8708684	1.80E-47	Hordeum vulgare
19	G526	4218536	3.60E-47	Triticum sp.
21	G545	4666359	8.30E-55	Datisca glomerata
21	G545	7228328	3.70E-52	Medicago sativa
21	G545	1763062	1.30E-51	Glycine max
21	G545	7206360	3.10E-44	Medicago truncatula
21	G545	7626808	9.60E-40	Gossypium arboreum
21	G545	439492	3.90E-39	Petunia x hybrida
21	G545	4382658	1.70E-38	Lycopersicon esculentum
21	G545	8486215	8.70E-38	Euphorbia esula
21	G545	7322653	6.80E-37	Lycopersicon hirsutum
21	G545	7785845	1.10E-33	Lotus japonicus
23	G561	2995461	5.60E-86	Sinapis alba
23	G561	633153	6.50E-83	Brassica napus

Figure 3C

SEQ ID No.	GID	Genbank NID	P-value	Species
23	G561	1033058	5.90E-65	Raphanus sativus
23	G561	2815304	2.10E-35	Spinacia oleracea
23	G561	1498300	1.60E-34	Petroselinum crispum
23	G561	169958	8.10E-32	Glycine max
23	G561	5381310	2.20E-30	Catharanthus roseus
23	G561	1155053	9.70E-28	Phaseolus vulgaris
23	G561	728627	1.90E-27	Nicotiana tabacum
23	G561	7565950	1.40E-21	Medicago truncatula
25	G664	1167483	4.90E-81	Lycopersicon esculentum
25	G664	7765706	6.30E-69	Medicago truncatula
25	G664	19052	9.30E-68	Hordeum vulgare
25	G664	7626566	4.00E-67	Gossypium arboreum
25	G664	5050757	2.60E-66	Gossypium hirsutum
25	G664	6850206	6.90E-66	Oryza sativa
25	G664	6667606	2.20E-63	Glycine max
25	G664	517492	9.30E-62	Zea mays
25	G664	9302672	1.50E-59	Sorghum bicolor
25	G664	5860031	9.20E-58	Pinus taeda
27	G682	309571	4.40E-08	Zea mays
27	G682	4396287	1.10E-05	Glycine max
27	G682	3857004	0.00051	Populus tremula x Populus tremuloides
27	G682	9410205	0.00085	Triticum aestivum
27	G682	8382118	0.0079	Gossypium arboreum
27	G682	2428139	0.017	Oryza sativa
27	G682	7339148	0.13	Lycopersicon esculentum
27	G682	9302672	0.32	Sorghum bicolor
27	G682	5048991	0.39	Gossypium hirsutum
27	G682	6555777	0.46	Pinus taeda
29	G911	4090113	6.10E-51	Brassica napus
29	G911	5893315	7.70E-25	Lycopersicon esculentum
29	G911	5048452	3.10E-23	Gossypium hirsutum
29	G911	9440241	1.90E-21	Glycine max
29	G911	6917169	1.80E-11	Lycopersicon pennellii
29	G911	9297970	3.20E-11	Sorghum bicolor
29	G911	7137594	4.90E-11	Zea mays
29	G911	9278447	4.60E-10	Lotus japonicus
29	G911	7560271	7.20E-10	Medicago truncatula
29	G911	5043346	4.50E-09	Sorghum halepense
31	G964	7624806	3.30E-72	Gossypium arboreum
31	G964	1234899	9.10E-66	Glycine max
31	G964	1149534	1.50E-61	Pimpinella brachycarpa
31	G964	8919872	3.40E-51	Capsella rubella
31	G964	992597	6.70E-51	Lycopersicon esculentum
31	G964	1235564	1.50E-38	Oryza sativa
31	G964	6605613	3.00E-32	Medicago truncatula
31	G964	1032371	4.50E-28	Helianthus annuus
31	G964	3868846	2.80E-25	Ceratopteris richardii
31	G964	8088109	6.40E-22	Sorghum bicolor
33	G394	8670502	7.90E-59	Glycine max
33	G394	3171738	2.00E-54	Craterostigma plantagineum
33	G394	1032371	1.10E-50	Helianthus annuus
33	G394	7624806	4.30E-47	Gossypium arboreum
33	G394	1160483	2.10E-46	Pimpinella brachycarpa

Figure 3D

SEQ ID No.	GID	Genbank NID	P-value	Species
33	G394	3868846	4.20E-45	Ceratopteris richardii
33	G394	992597	1.10E-44	Lycopersicon esculentum
33	G394	7558511	1.50E-44	Medicago truncatula
33	G394	8099247	6.20E-43	Oryza sativa
33	G394	8919872	1.20E-40	Capsella rubella
35	G489	6534956	4.40E-62	Lycopersicon esculentum
35	G489	9055852	2.60E-60	Medicago truncatula
35	G489	8382393	6.20E-51	Gossypium arboreum
35	G489	8789169	2.10E-50	Citrus x paradisi
35	G489	9252957	1.50E-47	Solanum tuberosum
35	G489	6918056	4.70E-47	Lycopersicon pennellii
35	G489	7590809	1.00E-46	Glycine max
35	G489	5257255	8.60E-43	Oryza sativa
35	G489	4152190	3.20E-41	Zea mays
35	G489	6069260	2.10E-39	Ceratodon purpureus
37	G463	6527230	4.90E-36	Lycopersicon esculentum
37	G463	9305572	5.50E-36	Sorghum bicolor
37	G463	3760881	1.20E-31	Oryza sativa
37	G463	6604917	1.30E-23	Medicago truncatula
37	G463	5058123	2.50E-21	Glycine max
37	G463	5044476	1.10E-19	Gossypium hirsutum
37	G463	9412603	1.70E-17	Triticum aestivum
37	G463	9419394	6.00E-17	Hordeum vulgare
37	G463	7624108	6.20E-17	Gossypium arboreum
37	G463	8547152	3.20E-16	Nicotiana tabacum
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39	G767	6732157	4.30E-51	Triticum monococcum
39	G767	9412602	6.90E-47	Triticum aestivum
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41	G765	1279639	4.30E-53	Petunia x hybrida
41	G765	4977542	2.00E-51	Oryza sativa
41	G765	4218536	2.00E-50	Triticum sp.
41	G765	6732159	2.00E-50	Triticum monococcum
41	G765	5049217	6.90E-50	Gossypium hirsutum
41	G765	9361647	4.50E-49	Triticum aestivum
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43	G197	7765706	1.50E-63	Medicago truncatula
43	G197	19052	8.90E-63	Hordeum vulgare
43	G197	5050757	1.60E-62	Gossypium hirsutum
43	G197	6850206	1.10E-61	Oryza sativa
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43	G197	517492	7.60E-59	Zea mays

Figure 3E

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45	G255	9302672	1.60E-56	Sorghum bicolor
45	G255	7721017	2.60E-55	Lotus japonicus
47	G1113	4090113	2.30E-36	Brassica napus
47	G1113	5048452	6.80E-12	Gossypium hirsutum
47	G1113	5893315	9.50E-11	Lycopersicon esculentum
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49	G398	1234899	6.90E-64	Glycine max
49	G398	1149534	6.20E-63	Pimpinella brachycarpa
49	G398	8919872	2.60E-47	Capsella rubella
49	G398	992597	1.10E-39	Lycopersicon esculentum
49	G398	1235564	7.70E-39	Oryza sativa
49	G398	6605613	1.70E-33	Medicago truncatula
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49	G398	3868846	1.60E-32	Ceratopteris richardii
49	G398	3171738	1.00E-27	Craterostigma plantagineum
51	G395	992597	5.30E-51	Lycopersicon esculentum
51	G395	7624806	2.00E-50	Gossypium arboreum
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51	G395	1165131	1.90E-48	Pimpinella brachycarpa
51	G395	3868846	3.40E-47	Ceratopteris richardii
51	G395	7415619	1.30E-41	Physcomitrella patens
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51	G395	1032371	3.30E-31	Helianthus annuus
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Page 8

MBI16 Sequence Listing.ST25

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Gln Trp Glu Lys Lys Leu Gln Thr Asp Ile Asn Met Ala Lys Gln Ala			
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Leu Phe Gln Ala Leu Ser Leu Asp Gln Pro Ser Ser Leu Ile Pro Pro			
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Asp Pro Asp Ser Pro Lys Pro His His His Ser Thr Thr Thr Tyr Ala			
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MBI16 Sequence Listing.ST25															
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Lys	Lys	Leu	Gln	Thr	Asp	Ile	Asn	Met	Ala	Lys	Gln	Ala	Leu	Phe	Gln
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Ala	Leu	Ser	Leu	Asp	Gln	Pro	Ser	Ser	Leu	Ile	Pro	Pro	Asp	Pro	Asp
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MBI16 Sequence Listing.ST25

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Asn Ser His His Gln Asn Asn Asn Asn Asn Asn His Gln His His Asn
175 180 185

cat cat cag ttt cag att ggg agt tcc aag tat ttg agt cca gct caa 989
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MBI16 Sequence Listing.ST25

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MBI16 Sequence Listing.ST25

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Ser Leu Thr Leu Gly Leu Gln Arg Asn Asp Gly Asn Gly Gly Val Ser			
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Gln Leu Leu His Asp Ile Val			
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MBI16 Sequence Listing.ST25

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Asn Asn Asn Asn Asn Asn His Gln His His Asn His His Gln Phe Gln
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Ile Gly Ser Ser Lys Tyr Leu Ser Pro Ala Gln Glu Leu Leu Ser Glu
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Phe Cys Ser Leu Gly Val Lys Glu Ser Asp Glu Glu Val Met Met Met
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Lys His Lys Lys Lys Gln Lys Gly Lys Gln Gln Glu Glu Trp Asp Thr
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Ser His His Ser Asn Asn Asp Gln His Asp Gln Ser Ala Thr Thr Ser
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Ser Lys Lys His Val Pro Pro Leu His Ser Leu Glu Phe Met Glu Leu
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Gln Lys Arg Lys Ala Lys Leu Leu Ser Met Leu Glu Glu Leu Lys Arg
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Leu Val Asp Ala His Pro Trp Arg Pro Gln Arg Gly Leu Pro Glu Arg
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Ala Val Thr Thr Leu Arg Ala Trp Leu Phe Glu His Phe Leu His Pro
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Tyr Pro Ser Asp Val Asp Lys His Ile Leu Ala Arg Gln Thr Gly Leu
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MBI16 Sequence Listing.ST25

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Asn Pro Thr Ser Lys Ser Gly His Asn Ser Thr His Gly Thr Met Ser
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Leu Gly Ser Thr Phe Asp Phe Ser Leu Tyr Gly Asn Gln Ala Val Thr
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Tyr Ala Gly Glu Gly Gly Pro Arg Gly Asp Val Ser Leu Thr Leu Gly
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Leu Gln Arg Asn Asp Gly Asn Gly Gly Val Ser Leu Ala Leu Ser Pro
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Val Thr Ala Gln Gly Gly Gln Leu Phe Tyr Gly Arg Asp His Ile Glu
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MBI16 Sequence Listing.ST25

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Val Val Gly Trp Pro Pro Ile Gly Leu His Arg Met Asn Ser Leu Val		
70	75 80 85	
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Asn Asn Gln Ala Met Lys Ala Ala Arg Ala Glu Glu Gly Asp Gly Glu		
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170	175 180	
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Met Phe His Gly Glu Cys Leu Ser Thr Arg		
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MBI16 Sequence Listing.ST25

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85 90 95

Glu Gly Asp Gly Glu Lys Lys Val Val Lys Asn Gly Glu Leu Lys Asp
100 105 110

Val Ser Met Lys Val Asn Pro Lys Val Gln Gly Leu Gly Phe Val Lys
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145 150 155 160

Gly Met Thr Gly Thr Thr Cys Arg Glu Thr Val Lys Pro Leu Arg Leu
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Leu Asp Gly Ser Ser Asp Phe Val Leu Thr Tyr Glu Asp Lys Gly Ile
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aatcattgat ggaaatgatt tgaaaaaaga gtaaagttaa tttttttatt ccttgtaatt 180

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Met Gly Asp Ser Asp Arg Asp Ser Gly Gly Gly Gln Asn Gly
1 5 10

aac aac cag aac gga cag tcc tcc ttg tct cca aga gag caa gac agg 277
Asn Asn Gln Asn Gly Gln Ser Ser Leu Ser Pro Arg Glu Gln Asp Arg
15 20 25 30

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Phe Leu Pro Ile Ala Asn Val Ser Arg Ile Met Lys Lys Ala Leu Pro
35 40 45

gcc aac gcc aag atc tct aaa gat gcc aaa gag acg atg cag gag tgt 373
Ala Asn Ala Lys Ile Ser Lys Asp Ala Lys Glu Thr Met Gln Glu Cys
50 55 60

gtc tcc gag ttc atc agc ttc gtc acc gga gaa gca tct gat aag tgt 421

MBI16 Sequence Listing.ST25

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Gln	Lys	Glu	Lys	Arg	Lys	Thr	Ile	Asn	Gly	Asp	Asp	Leu	Leu	Trp	Ala	
		80				85					90					
atg	act	act	cta	ggt	ttt	gag	gat	tat	gtt	gag	cca	ttg	aaa	gtt	tac	517
Met	Thr	Thr	Leu	Gly	Phe	Glu	Asp	Tyr	Val	Glu	Pro	Leu	Lys	Val	Tyr	
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Leu	Gln	Arg	Phe	Arg	Glu	Ile	Glu	Gly	Glu	Arg	Thr	Gly	Leu	Gly	Arg	
				115					120					125		
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Pro	Gln	Thr	Gly	Gly	Glu	Val	Gly	Glu	His	Gln	Arg	Asp	Ala	Val	Gly	
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gat	ggc	ggt	ggg	ttc	tac	ggt	ggt	ggt	ggt	ggg	atg	cag	tat	cac	caa	661
Asp	Gly	Gly	Gly	Phe	Tyr	Gly	Gly	Gly	Gly	Gly	Met	Gln	Tyr	His	Gln	
		145					150					155				
cat	cat	cag	ttt	ctt	cac	cag	cag	aac	cat	atg	tat	gga	gcc	aca	ggt	709
His	His	Gln	Phe	Leu	His	Gln	Gln	Asn	His	Met	Tyr	Gly	Ala	Thr	Gly	
		160				165					170					
ggc	ggt	agc	gac	agt	gga	ggt	gga	gct	gcc	tcc	ggt	agg	aca	agg	act	757
Gly	Gly	Ser	Asp	Ser	Gly	Gly	Gly	Ala	Ala	Ser	Gly	Arg	Thr	Arg	Thr	
					180				185						190	
taa	caaagattgg	tgaagtggat	ctctctctgt	atatagatac	ataaatacat											810
gtatacacat	gcctattttt	acgacccata	taaggtatct	atcatgtgat	agaacgaaca											870
ttggtgttgg	tgatgtaaaa	tcagatgtgc	attaagggtt	tagattttga	ggctgtgtaa											930
aagaagatca	agtgtgcttt	gttggacaat	aggattcact	aacgaatctg	cttcattgga											990
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Pro	Ile	Ala	Asn	Val	Ser	Arg	Ile	Met	Lys	Lys	Ala	Leu	Pro	Ala	Asn	
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Ala	Lys	Ile	Ser	Lys	Asp	Ala	Lys	Glu	Thr	Met	Gln	Glu	Cys	Val	Ser	
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MBI16 Sequence Listing.ST25

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Arg Phe Arg Glu Ile Glu Gly Glu Arg Thr Gly Leu Gly Arg Pro Gln
115 120 125

Thr Gly Gly Glu Val Gly Glu His Gln Arg Asp Ala Val Gly Asp Gly
130 135 140

Gly Gly Phe Tyr Gly Gly Gly Gly Met Gln Tyr His Gln His His
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Gln Phe Leu His Gln Gln Asn His Met Tyr Gly Ala Thr Gly Gly Gly
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cgcgctccgaa ttgattagga taggatcagg atcctcctca acaacctcct cctaattcct 180
cctccattca tagtaacaat aatattaaga aagagggtaa act atg tca gaa tta 235
Met Ser Glu Leu
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tta cag ttg cct cca ggt ttc cga ttt cac cct acc gat gaa gag ctt 283
Leu Gln Leu Pro Pro Gly Phe Arg Phe His Pro Thr Asp Glu Glu Leu
5 10 15 20
gtc atg cac tat ctc tgc cgc aaa tgt gcc tct cag tcc atc gcc gtt 331
Val Met His Tyr Leu Cys Arg Lys Cys Ala Ser Gln Ser Ile Ala Val
25 30 35
ccg atc atc gct gag atc gat ctc tac aaa tac gat cca tgg gag ctt 379
Pro Ile Ile Ala Glu Ile Asp Leu Tyr Lys Tyr Asp Pro Trp Glu Leu
40 45 50
cct ggt tta gcc ttg tat ggt gag aag gaa tgg tac ttc ttc tct ccc 427
Pro Gly Leu Ala Leu Tyr Gly Glu Lys Glu Trp Tyr Phe Phe Ser Pro
55 60 65
agg gac aga aaa tat ccc aac ggt tcg cgt cct aac cgg tcc gct ggt 475
Arg Asp Arg Lys Tyr Pro Asn Gly Ser Arg Pro Asn Arg Ser Ala Gly
70 75 80
tct ggt tac tgg aaa gct acc gga gct gat aaa ccg atc gga cta cct 523
Ser Gly Tyr Trp Lys Ala Thr Gly Ala Asp Lys Pro Ile Gly Leu Pro
85 90 95 100
aaa ccg gtc gga att aag aaa gct ctt gtt ttc tac gcc ggc aaa gct 571
Lys Pro Val Gly Ile Lys Lys Ala Leu Val Phe Tyr Ala Gly Lys Ala
105 110 115
cca aag gga gag aaa acc aat tgg atc atg cac gag tac cgt ctc gcc 619

MBI16 Sequence Listing.ST25

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Asp	Val	Asp	Arg	Ser	Val	Arg	Lys	Lys	Lys	Asn	Ser	Leu	Arg	Leu	Asp		
			135				140					145					
gat	tgg	gtt	ctc	tgc	cgg	att	tac	aac	aaa	aaa	gga	gct	acc	gag	agg	715	
Asp	Trp	Val	Leu	Cys	Arg	Ile	Tyr	Asn	Lys	Lys	Gly	Ala	Thr	Glu	Arg		
			150			155					160						
cgg	gga	cca	cgg	cct	cgg	gtt	gtt	tac	ggc	gac	gaa	atc	atg	gag	gag	763	
Arg	Gly	Pro	Pro	Pro	Pro	Val	Val	Tyr	Gly	Asp	Glu	Ile	Met	Glu	Glu		
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Lys	Pro	Lys	Val	Thr	Glu	Met	Val	Met	Pro	Pro	Pro	Pro	Gln	Gln	Thr		
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agt	gag	ttc	gcg	tat	ttc	gac	acg	tcg	gat	tcg	gtg	cgg	aag	ctg	cat	859	
Ser	Glu	Phe	Ala	Tyr	Phe	Asp	Thr	Ser	Asp	Ser	Val	Pro	Lys	Leu	His		
			200					205					210				
act	acg	gat	tcg	agt	tgc	tcg	gag	cag	gtg	gtg	tcg	cgg	gag	ttc	acg	907	
Thr	Thr	Asp	Ser	Ser	Cys	Ser	Glu	Gln	Val	Val	Ser	Pro	Glu	Phe	Thr		
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Ser	Glu	Val	Gln	Ser	Glu	Pro	Lys	Trp	Lys	Asp	Trp	Ser	Ala	Val	Ser		
			230			235					240						
aat	gac	aat	aac	aat	acc	ctt	gat	ttt	ggg	ttt	aat	tac	att	gat	gcc	1003	
Asn	Asp	Asn	Asn	Asn	Thr	Leu	Asp	Phe	Gly	Phe	Asn	Tyr	Ile	Asp	Ala		
					250				255					260			
acc	gtg	gat	aac	gcg	ttt	gga	gga	gga	ggg	agt	agt	aat	cag	atg	ttt	1051	
Thr	Val	Asp	Asn	Ala	Phe	Gly	Gly	Gly	Ser	Ser	Asn	Gln	Met	Phe			
				265				270					275				
cgg	cta	cag	gat	atg	ttc	atg	tac	atg	cag	aag	cct	tac	tag			1093	
Pro	Leu	Gln	Asp	Met	Phe	Met	Tyr	Met	Gln	Lys	Pro	Tyr					
			280				285										
aagggaattc	ctttcttgcc	gccgaaacgc	aacgcaaaac	gaccctcggt	tttgcgttta											1153	
tggcaacacg	agaccgtttt	atatggtcaa	tgagtgtgcc	gattcggcca	ttagatttct											1213	
gttcagtctt	cgtttattct	atagaccgtc	cgatttcaga	tcattccctaa	tcggacgggtg											1273	
gtcgttggat	gtatcagtag	tgtattactg	tgtaggttag	aagaaaatcc	acttggttctt											1333	
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 35 40 45

MBI16 Sequence Listing.ST25

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Phe Phe Ser Pro Arg Asp Arg Lys Tyr Pro Asn Gly Ser Arg Pro Asn
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          85          90          95

Ile Gly Leu Pro Lys Pro Val Gly Ile Lys Lys Ala Leu Val Phe Tyr
          100          105          110

Ala Gly Lys Ala Pro Lys Gly Glu Lys Thr Asn Trp Ile Met His Glu
          115          120          125

Tyr Arg Leu Ala Asp Val Asp Arg Ser Val Arg Lys Lys Lys Asn Ser
          130          135          140

Leu Arg Leu Asp Asp Trp Val Leu Cys Arg Ile Tyr Asn Lys Lys Gly
          145          150          155          160

Ala Thr Glu Arg Arg Gly Pro Pro Pro Pro Val Val Tyr Gly Asp Glu
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Ile Met Glu Glu Lys Pro Lys Val Thr Glu Met Val Met Pro Pro Pro
          180          185          190

Pro Gln Gln Thr Ser Glu Phe Ala Tyr Phe Asp Thr Ser Asp Ser Val
          195          200          205

Pro Lys Leu His Thr Thr Asp Ser Ser Cys Ser Glu Gln Val Val Ser
          210          215          220

Pro Glu Phe Thr Ser Glu Val Gln Ser Glu Pro Lys Trp Lys Asp Trp
          225          230          235          240

Ser Ala Val Ser Asn Asp Asn Asn Asn Thr Leu Asp Phe Gly Phe Asn
          245          250          255

Tyr Ile Asp Ala Thr Val Asp Asn Ala Phe Gly Gly Gly Gly Ser Ser
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Asn Gln Met Phe Pro Leu Gln Asp Met Phe Met Tyr Met Gln Lys Pro
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gggtttctga tattgttctt gttctcttga atctttatta cttgaaaaaac atataaagtg      180
atg gcg gtt gtg gtt gaa gaa ggt gtg gtg ttg aat cat gga ggt gaa      228
Met Ala Val Val Val Glu Glu Gly Val Val Leu Asn His Gly Gly Glu
1 5 10 15
gag ctt gtg gat ttg cca cct ggt ttc agg ttt cat cca aca gac gaa      276
Glu Leu Val Asp Leu Pro Pro Gly Phe Arg Phe His Pro Thr Asp Glu
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gag atc ata aca tgt tac ctt aag gag aag gtt tta aac agc cga ttc      324
Glu Ile Ile Thr Cys Tyr Leu Lys Glu Lys Val Leu Asn Ser Arg Phe
35 40 45
acg gct gtg gcc atg gga gaa gct gat ctc aac aag tgt gag cct tgg      372
Thr Ala Val Ala Met Gly Glu Ala Asp Leu Asn Lys Cys Glu Pro Trp
50 55 60
gat ttg cca aag agg gca aag atg ggg gag aaa gag ttc tac ttc ttc      420
Asp Leu Pro Lys Arg Ala Lys Met Gly Glu Lys Glu Phe Tyr Phe Phe
65 70 75 80
tgt caa agg gac agg aag tat ccg act ggg atg agg acg aac cgt gcg      468
Cys Gln Arg Asp Arg Lys Tyr Pro Thr Gly Met Arg Thr Asn Arg Ala
85 90 95
acg gag tca gga tac tgg aaa gcc acc ggg aag gat aag gag atc ttc      516
Thr Glu Ser Gly Tyr Trp Lys Ala Thr Gly Lys Asp Lys Glu Ile Phe
100 105 110
aaa ggc aaa ggt tgt ctc gtt ggg atg aag aaa aca ctt gtg ttt tat      564
Lys Gly Lys Gly Cys Leu Val Gly Met Lys Lys Thr Leu Val Phe Tyr
115 120 125
aga gga aga gct cca aaa ggt gaa aag act aat tgg gtc atg cat gaa      612
Arg Gly Arg Ala Pro Lys Gly Glu Lys Thr Asn Trp Val Met His Glu
130 135 140
tat cgt ctt gaa ggc aaa tat tcg tat tac aat ctc cca aaa tct gca      660
Tyr Arg Leu Glu Gly Lys Tyr Ser Tyr Tyr Asn Leu Pro Lys Ser Ala
145 150 155 160
agg gac gaa tgg gtc gtg tgt agg gtt ttt cac aag aac aat cct tct      708
Arg Asp Glu Trp Val Val Cys Arg Val Phe His Lys Asn Asn Pro Ser
165 170 175
acc aca acc caa cca atg acg aga ata ccc gtt gaa gat ttc aca agg      756
Thr Thr Thr Gln Pro Met Thr Arg Ile Pro Val Glu Asp Phe Thr Arg
180 185 190
atg gat tct cta gag aac att gat cat ctc cta gac ttc tca tct ctt      804
Met Asp Ser Leu Glu Asn Ile Asp His Leu Leu Asp Phe Ser Ser Leu
195 200 205
cct cct ctc ata gac ccg agt ttc atg agt caa acc gaa caa cca aac      852
Pro Pro Leu Ile Asp Pro Ser Phe Met Ser Gln Thr Glu Gln Pro Asn
210 215 220
ttc aaa ccc atc aac cct cca act tac gat atc tca tca cca atc caa      900
Phe Lys Pro Ile Asn Pro Pro Thr Tyr Asp Ile Ser Ser Pro Ile Gln
225 230 235 240
ccc cat cat ttc aat tct tac caa tca atc ttt aac cac cag gtt ttt      948
Pro His His Phe Asn Ser Tyr Gln Ser Ile Phe Asn His Gln Val Phe
245 250 255
ggg tct gct tcg ggc tct acg tac aac aac aac aac gag atg atc aag      996
Gly Ser Ala Ser Gly Ser Thr Tyr Asn Asn Asn Asn Glu Met Ile Lys
260 265 270

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MBI16 Sequence Listing.ST25

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Asp Val Asn Ala Asn Met Thr Thr Thr Thr Glu Val Ser Ser Gly Pro	
290 295 300	
gta atg aaa caa gaa atg ggg atg atg gga atg gtg aat ggt agc aag	1140
Val Met Lys Gln Glu Met Gly Met Met Gly Met Val Asn Gly Ser Lys	
305 310 315 320	
tcg tat gaa gat cta tgt gac ttg agg ggg gac ttg tgg gac ttc taa	1188
Ser Tyr Glu Asp Leu Cys Asp Leu Arg Gly Asp Leu Trp Asp Phe	
325 330 335	
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 35 40 45

Thr Ala Val Ala Met Gly Glu Ala Asp Leu Asn Lys Cys Glu Pro Trp
 50 55 60

Asp Leu Pro Lys Arg Ala Lys Met Gly Glu Lys Glu Phe Tyr Phe Phe
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Cys Gln Arg Asp Arg Lys Tyr Pro Thr Gly Met Arg Thr Asn Arg Ala
 85 90 95

Thr Glu Ser Gly Tyr Trp Lys Ala Thr Gly Lys Asp Lys Glu Ile Phe
 100 105 110

Lys Gly Lys Gly Cys Leu Val Gly Met Lys Lys Thr Leu Val Phe Tyr
 115 120 125

Arg Gly Arg Ala Pro Lys Gly Glu Lys Thr Asn Trp Val Met His Glu
 130 135 140

Tyr Arg Leu Glu Gly Lys Tyr Ser Tyr Tyr Asn Leu Pro Lys Ser Ala
 145 150 155 160

Arg Asp Glu Trp Val Val Cys Arg Val Phe His Lys Asn Asn Pro Ser

MBI16 Sequence Listing.ST25

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195 200 205

Pro Pro Leu Ile Asp Pro Ser Phe Met Ser Gln Thr Glu Gln Pro Asn
210 215 220

Phe Lys Pro Ile Asn Pro Pro Thr Tyr Asp Ile Ser Ser Pro Ile Gln
225 230 235 240

Pro His His Phe Asn Ser Tyr Gln Ser Ile Phe Asn His Gln Val Phe
245 250 255

Gly Ser Ala Ser Gly Ser Thr Tyr Asn Asn Asn Asn Glu Met Ile Lys
260 265 270

Met Glu Gln Ser Leu Val Ser Val Ser Gln Glu Thr Cys Leu Ser Ser
275 280 285

Asp Val Asn Ala Asn Met Thr Thr Thr Thr Glu Val Ser Ser Gly Pro
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Ala Leu Glu Ala Leu Thr Ser Pro Arg Leu Ala Ser Pro Ile Pro Pro
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ttg ttc gaa gat tct tca gtc ttc cat gga gtc gag cac tgg aca aag 153
Leu Phe Glu Asp Ser Ser Val Phe His Gly Val Glu His Trp Thr Lys
20 25 30

ggt aag cga tct aag aga tca aga tcc gat ttc cac cac caa aac ctc 201
Gly Lys Arg Ser Lys Arg Ser Arg Ser Asp Phe His His Gln Asn Leu
35 40 45

act gag gaa gag tat cta gct ttt tgc ctc atg ctt ctc gct cgc gac 249
Thr Glu Glu Glu Tyr Leu Ala Phe Cys Leu Met Leu Leu Ala Arg Asp
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MBI16 Sequence Listing.ST25

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70 75 80	
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Cys Ser Val Cys Asp Lys Thr Phe Ser Ser Tyr Gln Ala Leu Gly Gly	
85 90 95	
cac aag gca agc cac cgt aag aac tta tca cag act ctc tcc ggc gga	393
His Lys Ala Ser His Arg Lys Asn Leu Ser Gln Thr Leu Ser Gly Gly	
100 105 110	
gga gat gat cat tca acc tcg tcg gcg aca acc aca tcc gcc gtg act	441
Gly Asp Asp His Ser Thr Ser Ser Ala Thr Thr Ser Ala Val Thr	
115 120 125	
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Thr Gly Ser Gly Lys Ser His Val Cys Thr Ile Cys Asn Lys Ser Phe	
130 135 140 145	
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Pro Ser Gly Gln Ala Leu Gly Gly His Lys Arg Cys His Tyr Glu Gly	
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Asn Asn Asn Ile Asn Thr Ser Ser Val Ser Asn Ser Glu Gly Ala Gly	
165 170 175	
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Ser Thr Ser His Val Ser Ser Ser His Arg Gly Phe Asp Leu Asn Ile	
180 185 190	
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Pro Pro Ile Pro Glu Phe Ser Met Val Asn Gly Asp Asp Glu Val Met	
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Ser Pro Met Pro Ala Lys Lys Pro Arg Phe Asp Phe Pro Val Lys Leu	
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Gln Leu	
tgagagttgt gtaggaattt gttgactgta cataccaaat tggactttga ctgattccaa	838
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 35 40 45

Leu Thr Glu Glu Glu Tyr Leu Ala Phe Cys Leu Met Leu Leu Ala Arg
 50 55 60

Asp Asn Arg Gln Pro Pro Pro Pro Pro Ala Val Glu Lys Leu Ser Tyr
 65 70 75 80

MBI16 Sequence Listing.ST25

Lys Cys Ser Val Cys Asp Lys Thr Phe Ser Ser Tyr Gln Ala Leu Gly
85 90 95

Gly His Lys Ala Ser His Arg Lys Asn Leu Ser Gln Thr Leu Ser Gly
100 105 110

Gly Gly Asp Asp His Ser Thr Ser Ser Ala Thr Thr Thr Ser Ala Val
115 120 125

Thr Thr Gly Ser Gly Lys Ser His Val Cys Thr Ile Cys Asn Lys Ser
130 135 140

Phe Pro Ser Gly Gln Ala Leu Gly Gly His Lys Arg Cys His Tyr Glu
145 150 155 160

Gly Asn Asn Asn Ile Asn Thr Ser Ser Val Ser Asn Ser Glu Gly Ala
165 170 175

Gly Ser Thr Ser His Val Ser Ser Ser His Arg Gly Phe Asp Leu Asn
180 185 190

Ile Pro Pro Ile Pro Glu Phe Ser Met Val Asn Gly Asp Asp Glu Val
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Met Gly Ser Asn Glu Glu Gly Asn Pro
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act aac aac tct gat aag cca tcg caa gct gct gct cct gag cag agt 160
Thr Asn Asn Ser Asp Lys Pro Ser Gln Ala Ala Ala Pro Glu Gln Ser
10 15 20 25
aat gtt cat gtg tat cat cat gac tgg gct gct atg cag gca tat tat 208
Asn Val His Val Tyr His His Asp Trp Ala Ala Met Gln Ala Tyr Tyr
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ggg cct aga gtt ggt ata cct caa tat tac aac tca aat ttg gcg cct 256
Gly Pro Arg Val Gly Ile Pro Gln Tyr Tyr Asn Ser Asn Leu Ala Pro
45 50 55
ggt cat gct cca ccg cct tat atg tgg gcg tct cca tcg cca atg atg 304
Gly His Ala Pro Pro Pro Tyr Met Trp Ala Ser Pro Ser Pro Met Met
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MBI16 Sequence Listing.ST25																	
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ccc Pro	tca Ser	tct Ser	caa Gln 205	aac Asn	agt Ser	ctg Leu	cct Pro	ctt Leu 210	aga Arg	ggt Gly	gaa Glu	aat Asn	gag Glu 215	aaa Lys	ccc Pro	736	
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aac Asn	tct Ser 235	gct Ala	ggc Gly	atg Met	aac Asn	ggt Gly 240	gtg Val	cca Pro	cag Gln	cca Pro	tgg Trp 245	aat Asn	gaa Glu	aaa Lys	gag Glu	832	
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cta Leu	aac Asn	aat Asn 300	gag Glu	tct Ser	gag Glu	aaa Lys	cta Leu 305	cgg Arg	ctg Leu	gag Glu	aac Asn	gaa Glu 310	gct Ala	ata Ile	ttg Leu	1024	
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cga Arg 330	ggt Val	gat Asp	aag Lys	aac Asn	aac Asn 335	tct Ser	gta Val	tca Ser	ggc Gly	agc Ser 340	aaa Lys	act Thr	gtg Val	cag Gln	cat His 345	1120	
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ccgtggccgc aacaatgaga acccgatatt tcttcctttg gggtgtgatt gtaacttaaa																1228	
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MBI16 Sequence Listing.ST25

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Asp Trp Ala Ala Met Gln Ala Tyr Tyr Gly Pro Arg Val Gly Ile Pro
 35 40 45

Gln Tyr Tyr Asn Ser Asn Leu Ala Pro Gly His Ala Pro Pro Pro Tyr
 50 55 60

Met Trp Ala Ser Pro Ser Pro Met Met Ala Pro Tyr Gly Ala Pro Tyr
 65 70 75 80

Pro Pro Phe Cys Pro Pro Gly Gly Val Tyr Ala His Pro Gly Val Gln
 85 90 95

Met Gly Ser Gln Pro Gln Gly Pro Val Ser Gln Ser Ala Ser Gly Val
 100 105 110

Thr Thr Pro Leu Thr Ile Asp Ala Pro Ala Asn Ser Ala Gly Asn Ser
 115 120 125

Asp His Gly Phe Met Lys Lys Leu Lys Glu Phe Asp Gly Leu Ala Met
 130 135 140

Ser Ile Ser Asn Asn Lys Val Gly Ser Ala Glu His Ser Ser Ser Glu
 145 150 155 160

His Arg Ser Ser Gln Ser Ser Glu Asn Asp Gly Ser Ser Asn Gly Ser
 165 170 175

Asp Gly Asn Thr Thr Gly Gly Glu Gln Ser Arg Arg Lys Arg Arg Gln
 180 185 190

Gln Arg Ser Pro Ser Thr Gly Glu Arg Pro Ser Ser Gln Asn Ser Leu
 195 200 205

Pro Leu Arg Gly Glu Asn Glu Lys Pro Asp Val Thr Met Gly Thr Pro
 210 215 220

Val Met Pro Thr Ala Met Ser Phe Gln Asn Ser Ala Gly Met Asn Gly
 225 230 235 240

MBI16 Sequence Listing.ST25

Val Pro Gln Pro Trp Asn Glu Lys Glu Val Lys Arg Glu Lys Arg Lys
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Gln Ser Asn Arg Glu Ser Ala Arg Arg Ser Arg Leu Arg Lys Gln Ala
260 265 270

Glu Thr Glu Gln Leu Ser Val Lys Val Asp Ala Leu Val Ala Glu Asn
275 280 285

Met Ser Leu Arg Ser Lys Leu Gly Gln Leu Asn Asn Glu Ser Glu Lys
290 295 300

Leu Arg Leu Glu Asn Glu Ala Ile Leu Asp Gln Leu Lys Ala Gln Ala
305 310 315 320

Thr Gly Lys Thr Glu Asn Leu Ile Ser Arg Val Asp Lys Asn Asn Ser
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Ile Thr Asp Pro Val Ala Ala Ser
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Met Gly Arg Ser
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ccg tgc tgt gag aaa gct cac aca aac aaa gga gca tgg acg aaa gaa 163
Pro Cys Cys Glu Lys Ala His Thr Asn Lys Gly Ala Trp Thr Lys Glu
5 10 15 20

gag gac gag agg ctc gtc gcc tac att aaa gct cat gga gaa ggc tgc 211
Glu Asp Glu Arg Leu Val Ala Tyr Ile Lys Ala His Gly Glu Gly Cys
25 30 35

tgg aga tct ctc ccc aaa gcc gcc gga ctt ctt cgc tgt ggc aag agc 259
Trp Arg Ser Leu Pro Lys Ala Ala Gly Leu Leu Arg Cys Gly Lys Ser
40 45 50

tgc cgt ctc cgg tgg atc aac tat ctc cgg cct gac ctt aag cgt gga 307
Cys Arg Leu Arg Trp Ile Asn Tyr Leu Arg Pro Asp Leu Lys Arg Gly
55 60 65

aac ttc acc gag gaa gaa gac gaa ctc atc atc aag ctc cat agc ctt 355
Asn Phe Thr Glu Glu Glu Asp Glu Leu Ile Ile Lys Leu His Ser Leu
70 75 80

ctt ggc aac aaa tgg tgc ctt att gcc ggg aga tta ccg gga aga aca 403
Leu Gly Asn Lys Trp Ser Leu Ile Ala Gly Arg Leu Pro Gly Arg Thr
85 90 95 100

gat aac gag ata aag aac tat tgg aac acg cat ata cga aga aag ctt 451

MBI16 Sequence Listing.ST25

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Ile	Asn	Arg	Gly	Ile	Asp	Pro	Thr	Ser	His	Arg	Pro	Ile	Gln	Glu	Ser		
			120					125					130				
tca	gct	tct	caa	gat	tct	aaa	cct	aca	caa	cta	gaa	cca	gtt	acg	agt	547	
Ser	Ala	Ser	Gln	Asp	Ser	Lys	Pro	Thr	Gln	Leu	Glu	Pro	Val	Thr	Ser		
			135				140					145					
aat	acc	att	aat	atc	tca	ttc	act	tct	gct	cca	aag	gtc	gaa	acg	ttc	595	
Asn	Thr	Ile	Asn	Ile	Ser	Phe	Thr	Ser	Ala	Pro	Lys	Val	Glu	Thr	Phe		
	150					155					160						
cat	gaa	agt	ata	agc	ttt	ccg	gga	aaa	tca	gag	aaa	atc	tca	atg	ctt	643	
His	Glu	Ser	Ile	Ser	Phe	Pro	Gly	Lys	Ser	Glu	Lys	Ile	Ser	Met	Leu		
	165				170					175					180		
acg	ttc	aaa	gaa	gaa	aaa	gat	gag	tgc	cca	gtt	caa	gaa	aag	ttc	cca	691	
Thr	Phe	Lys	Glu	Glu	Lys	Asp	Glu	Cys	Pro	Val	Gln	Glu	Lys	Phe	Pro		
				185					190					195			
gat	ttg	aat	ctt	gag	ctc	aga	atc	agt	ctt	cct	gat	gat	gtt	gat	cgt	739	
Asp	Leu	Asn	Leu	Glu	Leu	Arg	Ile	Ser	Leu	Pro	Asp	Asp	Val	Asp	Arg		
			200					205					210				
ctt	caa	ggg	cat	gga	aag	tca	aca	acg	cca	cgt	tgt	ttc	aag	tgc	agc	787	
Leu	Gln	Gly	His	Gly	Lys	Ser	Thr	Thr	Pro	Arg	Cys	Phe	Lys	Cys	Ser		
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tta	ggg	atg	ata	aac	ggc	atg	gag	tgc	aga	tgc	gga	aga	atg	aga	tgc	835	
Leu	Gly	Met	Ile	Asn	Gly	Met	Glu	Cys	Arg	Cys	Gly	Arg	Met	Arg	Cys		
	230					235					240						
gat	gta	gtc	gga	ggt	agc	agc	aag	ggg	agt	gac	atg	agc	aat	gga	ttt	883	
Asp	Val	Val	Gly	Gly	Ser	Ser	Lys	Gly	Ser	Asp	Met	Ser	Asn	Gly	Phe		
	245				250				255					260			
gat	ttt	tta	ggg	ttg	gca	aag	aaa	gag	acc	act	tct	ctt	ttg	ggc	ttt	931	
Asp	Phe	Leu	Gly	Leu	Ala	Lys	Lys	Glu	Thr	Thr	Ser	Leu	Leu	Gly	Phe		
				265				270						275			
cga	agc	ttg	gag	atg	aaa	taa	tattgtcaaa	ttttaggcgt	aactgtacaa							982	
Arg	Ser	Leu	Glu	Met	Lys												
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Gly Glu Gly Cys Trp Arg Ser Leu Pro Lys Ala Ala Gly Leu Leu Arg
 35 40 45

Cys Gly Lys Ser Cys Arg Leu Arg Trp Ile Asn Tyr Leu Arg Pro Asp
 50 55 60

MBI16 Sequence Listing.ST25

Leu Lys Arg Gly Asn Phe Thr Glu Glu Glu Asp Glu Leu Ile Ile Lys
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 Leu His Ser Leu Leu Gly Asn Lys Trp Ser Leu Ile Ala Gly Arg Leu
 85 90 95
 Pro Gly Arg Thr Asp Asn Glu Ile Lys Asn Tyr Trp Asn Thr His Ile
 100 105 110
 Arg Arg Lys Leu Ile Asn Arg Gly Ile Asp Pro Thr Ser His Arg Pro
 115 120 125
 Ile Gln Glu Ser Ser Ala Ser Gln Asp Ser Lys Pro Thr Gln Leu Glu
 130 135 140
 Pro Val Thr Ser Asn Thr Ile Asn Ile Ser Phe Thr Ser Ala Pro Lys
 145 150 155 160
 Val Glu Thr Phe His Glu Ser Ile Ser Phe Pro Gly Lys Ser Glu Lys
 165 170 175
 Ile Ser Met Leu Thr Phe Lys Glu Glu Lys Asp Glu Cys Pro Val Gln
 180 185 190
 Glu Lys Phe Pro Asp Leu Asn Leu Glu Leu Arg Ile Ser Leu Pro Asp
 195 200 205
 Asp Val Asp Arg Leu Gln Gly His Gly Lys Ser Thr Thr Pro Arg Cys
 210 215 220
 Phe Lys Cys Ser Leu Gly Met Ile Asn Gly Met Glu Cys Arg Cys Gly
 225 230 235 240
 Arg Met Arg Cys Asp Val Val Gly Gly Ser Ser Lys Gly Ser Asp Met
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 Thr Ser Ser Ser Glu Glu Val Ser Ser Leu Glu Trp Glu Val Val Asn
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MBI16 Sequence Listing.ST25

atg agt caa gaa gaa gaa gat ttg gtc tct cga atg cat aag ctt gtc 144
Met Ser Gln Glu Glu Glu Asp Leu Val Ser Arg Met His Lys Leu Val
35 40 45

ggt gac agg tgg gaa ctg ata gct ggg agg atc cca gga aga acc gct 192
Gly Asp Arg Trp Glu Leu Ile Ala Gly Arg Ile Pro Gly Arg Thr Ala
50 55 60

gga gaa att gag agg ttt tgg gtc atg aaa aat tga 228
Gly Glu Ile Glu Arg Phe Trp Val Met Lys Asn
65 70 75

<210> 28
<211> 75
<212> PRT
<213> Arabidopsis thaliana

<400> 28

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1 5 10 15

Thr Ser Ser Ser Glu Glu Val Ser Ser Leu Glu Trp Glu Val Val Asn
20 25 30

Met Ser Gln Glu Glu Glu Asp Leu Val Ser Arg Met His Lys Leu Val
35 40 45

Gly Asp Arg Trp Glu Leu Ile Ala Gly Arg Ile Pro Gly Arg Thr Ala
50 55 60

Gly Glu Ile Glu Arg Phe Trp Val Met Lys Asn
65 70 75

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<222> (1)..(480)
<223> G911

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ata tta aag ata ctt tac gtc atc ggt ttc ttt aga gac atg gtc gat 96
Ile Leu Lys Ile Leu Tyr Val Ile Gly Phe Phe Arg Asp Met Val Asp
20 25 30

gct ctt tgt cct tac att ggt cta cct agt ttt cta gac cac aac gag 144
Ala Leu Cys Pro Tyr Ile Gly Leu Pro Ser Phe Leu Asp His Asn Glu
35 40 45

acc tct gga ccc gat ccg acc cga cac gct ctc tct acg tca gcg agt 192
Thr Ser Gly Pro Asp Pro Thr Arg His Ala Leu Ser Thr Ser Ala Ser
50 55 60

ctt gct aac gag ttg atc ccg gtg gtt cgg ttc tcg gat ctt ccg acc 240
Leu Ala Asn Glu Leu Ile Pro Val Val Arg Phe Ser Asp Leu Pro Thr
65 70 75 80

gat ccg gaa gat tgt tgt acg gtt tgt ttg tca gat ttt gag tcc gac 288
Asp Pro Glu Asp Cys Cys Thr Val Cys Leu Ser Asp Phe Glu Ser Asp

MBI16 Sequence Listing.ST25

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Asp Lys Val Arg Gln Leu Pro Lys Cys Gly His Val Phe His His His	100	105	110	
tgt tta gac cgt tgg atc gtt gac tac aac aag atg aaa tgt ccg gtt				384
Cys Leu Asp Arg Trp Ile Val Asp Tyr Asn Lys Met Lys Cys Pro Val	115	120	125	
tgt cgg cac cgg ttc tta ccg aaa gaa aag tac acg caa tgt gat tgg				432
Cys Arg His Arg Phe Leu Pro Lys Glu Lys Tyr Thr Gln Cys Asp Trp	130	135	140	
ggg tct ggt tca gat tgg ttt agt gat gaa gtg gaa agt acc aac taa				480
Gly Ser Gly Ser Asp Trp Phe Ser Asp Glu Val Glu Ser Thr Asn	145	150	155	

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 <212> PRT
 <213> Arabidopsis thaliana

<400> 30

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 20 25 30

Ala Leu Cys Pro Tyr Ile Gly Leu Pro Ser Phe Leu Asp His Asn Glu
 35 40 45

Thr Ser Gly Pro Asp Pro Thr Arg His Ala Leu Ser Thr Ser Ala Ser
 50 55 60

Leu Ala Asn Glu Leu Ile Pro Val Val Arg Phe Ser Asp Leu Pro Thr
 65 70 75 80

Asp Pro Glu Asp Cys Cys Thr Val Cys Leu Ser Asp Phe Glu Ser Asp
 85 90 95

Asp Lys Val Arg Gln Leu Pro Lys Cys Gly His Val Phe His His His
 100 105 110

Cys Leu Asp Arg Trp Ile Val Asp Tyr Asn Lys Met Lys Cys Pro Val
 115 120 125

Cys Arg His Arg Phe Leu Pro Lys Glu Lys Tyr Thr Gln Cys Asp Trp
 130 135 140

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ttcctgaaac tgttgagttc ttgtgaaagg aaataaaaaa c atg atg atg ggc aaa      176
                                     Met Met Met Gly Lys
                                     1           5

gaa gat cta ggt ttg agc cta agc tta ggg ttt tca caa aat cac aat      224
Glu Asp Leu Gly Leu Ser Leu Ser Leu Gly Phe Ser Gln Asn His Asn
                                     10           20

cct ctt cag atg aat ctg aat cct aac tct tca tta tca aac aat ctc      272
Pro Leu Gln Met Asn Leu Asn Pro Asn Ser Ser Leu Ser Asn Asn Leu
                                     25           35

cag aga ctc cca tgg aac caa aca ttc gat cct aca tca gat ctt cgc      320
Gln Arg Leu Met Pro Trp Asn Gln Thr Phe Asp Pro Thr Ser Asp Leu Arg
                                     40           50

aag ata gac gtg aac agt ttt cca tca acg gtt aac tgc gag gaa gac      368
Lys Ile Asp Val Asn Ser Phe Pro Ser Thr Val Asn Cys Glu Glu Asp
                                     55           65

aca gga gtt tcg tca cca aac agt acg atc tca agc acc att agc ggg      416
Thr Gly Val Ser Ser Pro Asn Ser Thr Ile Ser Ser Thr Ile Ser Gly
                                     70           85

aag aga agt gag aga gaa gga atc tcc gga acc ggc gtt ggc tcc ggc      464
Lys Arg Ser Glu Arg Glu Gly Ile Ser Gly Thr Gly Val Gly Ser Gly
                                     90          100

gac gat cac gag atc act ccg gat cga ggg tac tca cgt gga acc      512
Asp Asp His Asp Glu Ile Thr Pro Asp Arg Gly Tyr Ser Arg Gly Thr
                                     105          115

tca gat gaa gaa gaa gac ggg ggc gaa acg tcg agg aag aag ctc agg      560
Ser Asp Glu Glu Glu Asp Gly Gly Glu Thr Ser Arg Lys Lys Leu Arg
                                     120          125

tta tca aaa gat cag tct gct ttt ctc gaa gag act ttc aaa gaa cac      608
Leu Ser Lys Asp Gln Ser Ala Phe Leu Glu Glu Thr Phe Lys Glu His
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aac act ctc aat ccc aaa cag aag cta gct ttg gct aag aag ctg aac      656
Asn Thr Leu Asn Pro Lys Gln Lys Leu Ala Leu Ala Lys Lys Leu Asn
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ttg acg gca aga caa gtg gaa gtg tgg ttc caa aac aga aga gct aga      704
Leu Thr Ala Arg Gln Val Glu Val Trp Phe Gln Asn Arg Arg Ala Arg
                                     170          180

acc aag tta aag caa acg gag gta gat tgc gaa tac ttg aaa cgg tgc      752
Thr Lys Leu Lys Gln Thr Glu Val Asp Cys Glu Tyr Leu Lys Arg Cys
                                     185          195

gta gag aag cta acg gaa gag aac cgg aga ctt cag aaa gag gct atg      800
Val Glu Lys Leu Thr Glu Glu Asn Arg Arg Leu Gln Lys Glu Ala Met
                                     200          210

gag ctt cga act ctc aag ctg tct cca caa ttc tac ggt cag atg act      848
Glu Leu Arg Thr Leu Lys Leu Ser Pro Gln Phe Tyr Gly Gln Met Thr
                                     215          225

cca cca act aca ctc atc atg tgt cct tcg tgc gag cgt gta gct ggt      896
Pro Pro Thr Thr Leu Ile Met Cys Pro Ser Cys Glu Arg Val Ala Gly
                                     230          245

cca tca tca tcg aac cat cac cac aat cac agg ccg gtt tcg att aac      944
Pro Ser Ser Ser Asn His His His Asn His Arg Pro Val Ser Ile Asn
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MBI16 Sequence Listing.ST25

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Pro Trp Ile Ala Cys Ala Gly Gln Val Ala His Gly Leu Asn Phe Glu
      265                      270                      275

gcc ttg cgt cca cga tcg taa ttttagtggtg tgggggaagg gtgttttggg      1043
Ala Leu Arg Pro Arg Ser
      280

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ccttctcatg aactagtcac atgtatgatg caaccttaaa aatatttcaa gtagcaaaac      1163

ttaattacaa acttgctata ttaaccacaaa attatgaaaa aaaaaaaaaa aaaaaaaaaa      1221

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      20                      25                      30

Leu Ser Asn Asn Leu Gln Arg Leu Pro Trp Asn Gln Thr Phe Asp Pro
      35                      40                      45

Thr Ser Asp Leu Arg Lys Ile Asp Val Asn Ser Phe Pro Ser Thr Val
50                      55                      60

Asn Cys Glu Glu Asp Thr Gly Val Ser Ser Pro Asn Ser Thr Ile Ser
65                      70                      75                      80

Ser Thr Ile Ser Gly Lys Arg Ser Glu Arg Glu Gly Ile Ser Gly Thr
      85                      90                      95

Gly Val Gly Ser Gly Asp Asp His Asp Glu Ile Thr Pro Asp Arg Gly
100                      105                      110

Tyr Ser Arg Gly Thr Ser Asp Glu Glu Glu Asp Gly Gly Glu Thr Ser
115                      120                      125

Arg Lys Lys Leu Arg Leu Ser Lys Asp Gln Ser Ala Phe Leu Glu Glu
130                      135                      140

Thr Phe Lys Glu His Asn Thr Leu Asn Pro Lys Gln Lys Leu Ala Leu
145                      150                      155                      160

Ala Lys Lys Leu Asn Leu Thr Ala Arg Gln Val Glu Val Trp Phe Gln
165                      170                      175

Asn Arg Arg Ala Arg Thr Lys Leu Lys Gln Thr Glu Val Asp Cys Glu
180                      185                      190

Tyr Leu Lys Arg Cys Val Glu Lys Leu Thr Glu Glu Asn Arg Arg Leu
195                      200                      205

Gln Lys Glu Ala Met Glu Leu Arg Thr Leu Lys Leu Ser Pro Gln Phe

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Page 36

MBI16 Sequence Listing.ST25

155	160	165	170	
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Phe Gln Asn Arg Arg Ala Arg Thr Lys Leu Lys Gln Thr Glu Val Asp	175	180	185	
tgt gag ttt ttg aag aaa tgt tgc gag act tta acg gat gag aat aga				687
Cys Glu Phe Leu Lys Lys Cys Cys Glu Thr Leu Thr Asp Glu Asn Arg	190	195	200	
agg ctt caa aaa gag ctt caa gac ctt aag gct tta aaa ttg tct caa				735
Arg Leu Gln Lys Glu Leu Gln Asp Leu Lys Ala Leu Lys Leu Ser Gln	205	210	215	
ccg ttt tac atg cac atg ccg gcg gcg act ttg act atg tgc cct tct				783
Pro Phe Tyr Met His Met Pro Ala Ala Thr Leu Thr Met Cys Pro Ser	220	225	230	
tgt gag aga ctc ggc ggt ggt ggt gtc gga gga gat acg acg gcg gtt				831
Cys Glu Arg Leu Gly Gly Gly Gly Val Gly Gly Asp Thr Thr Ala Val	235	240	245	250
gat gaa gaa acg gcg aaa gga gct ttc tcc atc gtc aca aag cct cgt				879
Asp Glu Glu Thr Ala Lys Gly Ala Phe Ser Ile Val Thr Lys Pro Arg	255	260	265	
ttc tat aac cct ttc act aat cct tct gca gca tgt tag ttacttatta				928
Phe Tyr Asn Pro Phe Thr Asn Pro Ser Ala Ala Cys	270	275		
gttattttaat tcttttttgtt ggtttttttt ttgtttctta aatcaaatta ggaattagtt				988
agaagataaaa tcccaggga aaaatattac gttgaaattg gggggaaatg gggatatagtc				1048
tttatagata agactcttca acgattccac tttatttttc ggtgggattg ttggttgatg				1108
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aaataataaaa tatattattt g				1249

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 20 25 30

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 35 40 45

Ser Leu Ser Gly Glu Ser Tyr Lys Ile Lys Thr Gly Ala Gly Ala Gly
 50 55 60

Asp Gln Ile Cys Arg Gln Thr Ser Ser His Ser Gly Ile Ser Ser Phe
 65 70 75 80

Ser Ser Gly Arg Val Lys Arg Glu Arg Glu Ile Ser Gly Gly Asp Gly
 85 90 95

Glu Glu Glu Ala Glu Glu Thr Thr Glu Arg Val Val Cys Ser Arg Val

MBI16 Sequence Listing.ST25

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Ser Asp Asp His Asp Asp Glu	Glu Gly Val Ser Ala Arg	Lys Lys Leu	
115	120	125	
Arg Leu Thr Lys Gln Gln Ser	Ala Leu Leu Glu Asp Asn Phe	Lys Leu	
130	135	140	
His Ser Thr Leu Asn Pro Lys	Gln Lys Gln Ala Leu Ala Arg	Gln Leu	
145	150	155	160
Asn Leu Arg Pro Arg Gln Val	Glu Val Trp Phe Gln Asn Arg	Arg Ala	
165	170	175	
Arg Thr Lys Leu Lys Gln Thr	Glu Val Asp Cys Glu Phe Leu	Lys Lys	
180	185	190	
Cys Cys Glu Thr Leu Thr Asp	Glu Asn Arg Arg Leu Gln	Lys Glu Leu	
195	200	205	
Gln Asp Leu Lys Ala Leu Lys	Leu Ser Gln Pro Phe Tyr Met	His Met	
210	215	220	
Pro Ala Ala Thr Leu Thr Met	Cys Pro Ser Cys Glu Arg Leu	Gly Gly	
225	230	235	240
Gly Gly Val Gly Gly Asp Thr	Thr Ala Val Asp Glu Glu Thr	Ala Lys	
245	250	255	
Gly Ala Phe Ser Ile Val Thr	Lys Pro Arg Phe Tyr Asn Pro	Phe Thr	
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Asn Pro Ser Ala Ala Cys			
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tac caa acc aac ccg atg agc acc act gct gct act gta gca gga ggt		101
Tyr Gln Thr Asn Pro Met Ser Thr Thr Ala Ala Thr Val Ala Gly Gly		
10 15 20		
gcg gca caa cca ggc cag ctg gcg ttc cac cag atc cat cag cag cag		149
Ala Ala Gln Pro Gly Gln Leu Ala Phe His Gln Ile His Gln Gln Gln		
25 30 35		
cag cag caa cag ctg gca cag cag ctt caa gca ttt tgg gag aac caa		197
Gln Gln Gln Gln Leu Ala Gln Gln Leu Gln Ala Phe Trp Glu Asn Gln		
40 45 50 55		

MBI16 Sequence Listing.ST25

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Phe Lys Glu Ile Glu Lys Thr Thr Asp Phe Lys Asn His Ser Leu Pro	
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Leu Ala Arg Ile Lys Lys Ile Met Lys Ala Asp Glu Asp Val Arg Met	
75 80 85	
atc tcg gct gag gcg ccg gtc gtg ttt gca agg gcc tgt gag atg ttc	341
Ile Ser Ala Glu Ala Pro Val Val Phe Ala Arg Ala Cys Glu Met Phe	
90 95 100	
atc ctg gag ctg aca ctc agg tcg tgg aac cac act gag gag aat aag	389
Ile Leu Glu Leu Thr Leu Arg Ser Trp Asn His Thr Glu Glu Asn Lys	
105 110 115	
agg cgg acg ttg cag aag aac gat att gct gct gct gtg act aga acc	437
Arg Arg Thr Leu Gln Lys Asn Asp Ile Ala Ala Val Thr Arg Thr	
120 125 130 135	
gat att ttt gat ttc ctt gtg gat att gtt ccc cgg gag gat ctc cga	485
Asp Ile Phe Asp Phe Leu Val Asp Ile Val Pro Arg Glu Asp Leu Arg	
140 145 150	
gat gaa gtc ttg gga agt att ccg agg ggc act gtc ccg gaa gct gct	533
Asp Glu Val Leu Gly Ser Ile Pro Arg Gly Thr Val Pro Glu Ala Ala	
155 160 165	
gct gct ggt tac ccg tat gga tac ttg cct gca gga act gct cca ata	581
Ala Ala Gly Tyr Pro Tyr Gly Tyr Leu Pro Ala Gly Thr Ala Pro Ile	
170 175 180	
gga aat ccg gga atg gtt atg ggt aat ccc ggt ggt gcg tat cca cct	629
Gly Asn Pro Gly Met Val Met Gly Asn Pro Gly Gly Ala Tyr Pro Pro	
185 190 195	
aat cct tat atg ggt caa cca atg tgg caa caa cag gca cct gac caa	677
Asn Pro Tyr Met Gly Gln Pro Met Trp Gln Gln Gln Ala Pro Asp Gln	
200 205 210 215	
cct gac cag gaa aat tag caagaaactg tgagtcttcc agcttcgcgg	725
Pro Asp Gln Glu Asn	
220	
ccgctctaga caggcctcgt accggatcct ctagctagag ctttcgctcg tatcatcggt	785
ttcgacaacg ttcgtcaagt tcaatgcac agtttcattg cgcacacacc agaatcctac	845
tgagtttgag tattatggca ttgggaaaac tgtttttctt gtccatttgt tgtgcttgta	905
atttactgtg ttttttattc gggttttcgct atcgaactgt gaaatggaaa tggatggaga	965
agagttaatg aatgatatgg cctttttgttc attctcaa ataatattatt tggtttttct	1025
cttatttgtg gggatgaatt tgaaattata agagatatgc aaacattttg tttgagtaaa	1085
atgtgc aaat cgtggcctct aatgacccga agttaatatg aggagtaaaa cacttgtagg	1145
tg	1147
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Ala Ala Thr Val Ala Gly Gly Ala Ala Gln Pro Gly Gln Leu Ala Phe	
20 25 30	

MBI16 Sequence Listing.ST25

His Gln Ile His Gln Gln Gln Gln Gln Gln Gln Leu Ala Gln Gln Leu
 35 40 45
 Gln Ala Phe Trp Glu Asn Gln Phe Lys Glu Ile Glu Lys Thr Thr Asp
 50 55 60
 Phe Lys Asn His Ser Leu Pro Leu Ala Arg Ile Lys Lys Ile Met Lys
 65 70 75 80
 Ala Asp Glu Asp Val Arg Met Ile Ser Ala Glu Ala Pro Val Val Phe
 85 90 95
 Ala Arg Ala Cys Glu Met Phe Ile Leu Glu Leu Thr Leu Arg Ser Trp
 100 105 110
 Asn His Thr Glu Glu Asn Lys Arg Arg Thr Leu Gln Lys Asn Asp Ile
 115 120 125
 Ala Ala Ala Val Thr Arg Thr Asp Ile Phe Asp Phe Leu Val Asp Ile
 130 135 140
 Val Pro Arg Glu Asp Leu Arg Asp Glu Val Leu Gly Ser Ile Pro Arg
 145 150 155 160
 Gly Thr Val Pro Glu Ala Ala Ala Ala Gly Tyr Pro Tyr Gly Tyr Leu
 165 170 175
 Pro Ala Gly Thr Ala Pro Ile Gly Asn Pro Gly Met Val Met Gly Asn
 180 185 190
 Pro Gly Gly Ala Tyr Pro Pro Asn Pro Tyr Met Gly Gln Pro Met Trp
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 Gln Gln Gln Ala Pro Asp Gln Pro Asp Gln Glu Asn
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 ctttcaaaag actctttctt tcttttggtg tgattttgga ttctagggtc ctctttcttt 180
 tagtggggtt ttgttggtgt tggttggtgc tctctg atg att act gaa ctt gag 234
 Met Ile Thr Glu Leu Glu
 1 5
 atg ggg aaa ggt gag agt gag ctt gag ctt ggt cta ggg ctg agt ctt 282
 Met Gly Lys Gly Glu Ser Glu Leu Glu Leu Gly Leu Gly Leu Ser Leu
 10 15 20

MBI16 Sequence Listing.ST25

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tgg gga gag cgt gga agg ctt ttg acg gct aag gat ttt cct tct gtt      378
Trp Gly Glu Arg Gly Arg Leu Leu Thr Ala Lys Asp Phe Pro Ser Val
    40                               45                               50

ggg tct aaa cgt gct gct gat tct gct tct cat gct ggt tca tct cct      426
Gly Ser Lys Arg Ala Ala Asp Ser Ala Ser His Ala Gly Ser Ser Pro
    55                               60                               65                               70

cct cgt tca agt caa gtt gtt gga tgg cct cct ata ggg tca cac agg      474
Pro Arg Ser Ser Gln Val Val Gly Trp Pro Pro Ile Gly Ser His Arg
    75                               80                               85

atg aac agt ttg gtt aat aac caa gct aca aag tca gca aga gaa gaa      522
Met Asn Ser Leu Val Asn Asn Gln Ala Thr Lys Ser Ala Arg Glu Glu
    90                               95                               100

gaa gaa gct ggt aag aag aaa gtg aaa gat gat gaa cct aaa gat gtg      570
Glu Glu Ala Gly Lys Lys Lys Val Lys Asp Asp Glu Pro Lys Asp Val
    105                              110                              115

aca aag aaa gtg aat ggg aaa gta caa gtt gga ttt att aag gtg aac      618
Thr Lys Lys Val Asn Gly Lys Val Gln Val Gly Phe Ile Lys Val Asn
    120                              125                              130

atg gat gga gtt gct ata gga aga aaa gtg gat ttg aat gct cat tct      666
Met Asp Gly Val Ala Ile Gly Arg Lys Val Asp Leu Asn Ala His Ser
    135                              140                              145                              150

tct tac gag aat ttg gcg caa aca ttg gaa gat atg ttc ttt cgc act      714
Ser Tyr Glu Asn Leu Ala Gln Thr Leu Glu Asp Met Phe Phe Arg Thr
    155                              160                              165

aat ccg ggt act gtc ggg tta acc agt cag ttc act aaa ccg ttg agg      762
Asn Pro Gly Thr Val Gly Leu Thr Ser Gln Phe Thr Lys Pro Leu Arg
    170                              175                              180

ctt tta gat gga tcg tct gag ttt gta ctt act tat gaa gat aag gaa      810
Leu Leu Asp Gly Ser Ser Glu Phe Val Leu Thr Tyr Glu Asp Lys Glu
    185                              190                              195

gga gat tgg atg ctt gtt ggt gat gtt cca tgg aga atg ttc atc aac      858
Gly Asp Trp Met Leu Val Gly Asp Val Pro Trp Arg Met Phe Ile Asn
    200                              205                              210

tcg gtg aaa agg cta cgt gtg atg aaa acc tct gaa gct aat gga ctc      906
Ser Val Lys Arg Leu Arg Val Met Lys Thr Ser Glu Ala Asn Gly Leu
    215                              220                              225                              230

gct gca cga aat caa gaa cca aac gag aga cag cga aag cag ccg gtt      954
Ala Ala Arg Asn Gln Glu Pro Asn Glu Arg Gln Arg Lys Gln Pro Val
    235                              240                              245

tag atctcttttc gacgttacgg tggttacaggt tttatatattt ggggttttgc      1007

aagtctgaga tacttctgaa gcaagcataa gctagattga tcttatatcc agtttgtgta      1067

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MBI16 Sequence Listing.ST25

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 20 25 30
 Ser Gly Gly Gly Gly Ala Trp Gly Glu Arg Gly Arg Leu Leu Thr Ala
 35 40 45
 Lys Asp Phe Pro Ser Val Gly Ser Lys Arg Ala Ala Asp Ser Ala Ser
 50 55 60
 His Ala Gly Ser Ser Pro Pro Arg Ser Ser Gln Val Val Gly Trp Pro
 65 70 75 80
 Pro Ile Gly Ser His Arg Met Asn Ser Leu Val Asn Asn Gln Ala Thr
 85 90 95
 Lys Ser Ala Arg Glu Glu Glu Glu Ala Gly Lys Lys Lys Val Lys Asp
 100 105 110
 Asp Glu Pro Lys Asp Val Thr Lys Lys Val Asn Gly Lys Val Gln Val
 115 120 125
 Gly Phe Ile Lys Val Asn Met Asp Gly Val Ala Ile Gly Arg Lys Val
 130 135 140
 Asp Leu Asn Ala His Ser Ser Tyr Glu Asn Leu Ala Gln Thr Leu Glu
 145 150 155 160
 Asp Met Phe Phe Arg Thr Asn Pro Gly Thr Val Gly Leu Thr Ser Gln
 165 170 175
 Phe Thr Lys Pro Leu Arg Leu Leu Asp Gly Ser Ser Glu Phe Val Leu
 180 185 190
 Thr Tyr Glu Asp Lys Glu Gly Asp Trp Met Leu Val Gly Asp Val Pro
 195 200 205
 Trp Arg Met Phe Ile Asn Ser Val Lys Arg Leu Arg Val Met Lys Thr
 210 215 220
 Ser Glu Ala Asn Gly Leu Ala Ala Arg Asn Gln Glu Pro Asn Glu Arg
 225 230 235 240
 Gln Arg Lys Gln Pro Val
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MBI16 Sequence Listing.ST25

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Met Met Lys Ser Gly Ala Asp Leu Gln Phe Pro Pro
1 5 10

gga ttt aga ttt cat cct acg gat gag gag cta gtc ctc atg tat ctc 159
Gly Phe Arg Phe His Pro Thr Asp Glu Glu Leu Val Leu Met Tyr Leu
15 20 25

tgt cgt aaa tgc gcg tcg cag ccg atc cct gct ccg att atc acc gaa 207
Cys Arg Lys Cys Ala Ser Thr Pro Ile Pro Ala Pro Ile Ile Thr Glu
30 35 40

ctc gat ttg tac cga tat gat cct tgg gac ctt ccc gac atg gct ttg 255
Leu Asp Leu Tyr Arg Tyr Asp Pro Trp Asp Leu Pro Asp Met Ala Leu
45 50 55 60

tac ggt gaa aag gag tgg tat ttt ttc tca cca aga gat cga aag tat 303
Tyr Gly Glu Lys Glu Trp Tyr Phe Phe Ser Pro Arg Asp Arg Lys Tyr
65 70 75

cca aac ggt tca aga ccc aac cgt gca gct ggt act gga tat tgg aaa 351
Pro Asn Gly Ser Arg Pro Asn Arg Ala Ala Gly Thr Gly Tyr Trp Lys
80 85 90

gct acc gga gct gat aaa cca ata ggt cgt cct aaa ccg gtt ggt att 399
Ala Thr Gly Ala Asp Lys Pro Ile Gly Arg Pro Lys Pro Val Gly Ile
95 100 105

aag aag gct cta gtg ttt tac tcg gga aaa cct cca aat gga gag aaa 447
Lys Lys Ala Leu Val Phe Tyr Ser Gly Lys Pro Pro Asn Gly Glu Lys
110 115 120

acc aat tgg att atg cac gaa tac cgg ctc gct gac gtt gac cgg tcg 495
Thr Asn Trp Ile Met His Glu Tyr Arg Leu Ala Asp Val Asp Arg Ser
125 130 135 140

ggt cgt aag aaa aac agt cta aga ttg gac gat tgg gta ttg tgt cgt 543
Val Arg Lys Lys Asn Ser Leu Arg Leu Asp Asp Trp Val Leu Cys Arg
145 150 155

ata tat aac aag aaa ggt gtc atc gag aag cga cga agc gat atc gag 591
Ile Tyr Asn Lys Lys Gly Val Ile Glu Lys Arg Arg Ser Asp Ile Glu
160 165 170

gac ggg tta aag cct gtg act gac acg tgt cca ccg gaa tct gtg gcg 639
Asp Gly Leu Lys Pro Val Thr Asp Thr Cys Pro Pro Glu Ser Val Ala
175 180 185

aga ttg atc tcc ggc tcg gag caa gcg gtg tca ccg gaa ttc acg tgt 687
Arg Leu Ile Ser Gly Ser Glu Gln Ala Val Ser Pro Glu Phe Thr Cys
190 195 200

agc aac ggt ccg ttg agt aat gcc ctt gat ttt ccg ttt aat tac gta 735
Ser Asn Gly Arg Leu Ser Asn Ala Leu Asp Phe Pro Phe Asn Tyr Val
205 210 215 220

gat gcc atc gcc gat aac gag att gtg tca ccg cta ttg ggc ggg aat 783
Asp Ala Ile Ala Asp Asn Glu Ile Val Ser Arg Leu Leu Gly Gly Asn
225 230 235

cag atg tgg tcg acg acg ctt gat cca ctt gtg gtt agg cag gga act 831
Gln Met Trp Ser Thr Thr Leu Asp Pro Leu Val Val Arg Gln Gly Thr
240 245 250

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Phe

ttttcgcaacg tgtcgggc 905

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MBI16 Sequence Listing.ST25

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Ala Ser Gln Pro Ile Pro Ala Pro Ile Ile Thr Glu Leu Asp Leu Tyr
35     40     45
Arg Tyr Asp Pro Trp Asp Leu Pro Asp Met Ala Leu Tyr Gly Glu Lys
50     55     60
Glu Trp Tyr Phe Phe Ser Pro Arg Asp Arg Lys Tyr Pro Asn Gly Ser
65     70     75     80
Arg Pro Asn Arg Ala Ala Gly Thr Gly Tyr Trp Lys Ala Thr Gly Ala
85     90     95
Asp Lys Pro Ile Gly Arg Pro Lys Pro Val Gly Ile Lys Lys Ala Leu
100    105    110
Val Phe Tyr Ser Gly Lys Pro Pro Asn Gly Glu Lys Thr Asn Trp Ile
115    120    125
Met His Glu Tyr Arg Leu Ala Asp Val Asp Arg Ser Val Arg Lys Lys
130    135    140
Asn Ser Leu Arg Leu Asp Asp Trp Val Leu Cys Arg Ile Tyr Asn Lys
145    150    155    160
Lys Gly Val Ile Glu Lys Arg Arg Ser Asp Ile Glu Asp Gly Leu Lys
165    170    175
Pro Val Thr Asp Thr Cys Pro Pro Glu Ser Val Ala Arg Leu Ile Ser
180    185    190
Gly Ser Glu Gln Ala Val Ser Pro Glu Phe Thr Cys Ser Asn Gly Arg
195    200    205
Leu Ser Asn Ala Leu Asp Phe Pro Phe Asn Tyr Val Asp Ala Ile Ala
210    215    220
Asp Asn Glu Ile Val Ser Arg Leu Leu Gly Gly Asn Gln Met Trp Ser
225    230    235    240
Thr Thr Leu Asp Pro Leu Val Val Arg Gln Gly Thr Phe
245    250

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<210> 41
<211> 1479
<212> DNA
<213> Arabidopsis thaliana

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MBI16 Sequence Listing.ST25

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cgatctcctc aaaaagttat tgttttcttg aaggattttt cttgttcttg atcaagcata      180
catatatata g atg gtg gaa gaa ggc ggc gta gtt gtg aat caa gga gga      230
          Met Val Glu Glu Gly Gly Val Val Val Asn Gln Gly Gly
          1          5          10

gat cag gag gtg gtg gat ttg cct ccg ggg ttt cgg ttt cac cct act      278
Asp Gln Glu Val Val Asp Leu Pro Pro Gly Phe Arg Phe His Pro Thr
    15          20          25

gat gaa gag ata ata act cac tac ctc aaa gag aag gtc ttc aac atc      326
Asp Glu Glu Ile Ile act His Tyr Leu Lys Glu Lys Val Phe Asn Ile
    30          35          40          45

cga ttt acc gcg gca gcg att ggt caa gcc gac ctc aac aag aac gag      374
Arg Phe Thr Ala Ala Ala Ile Gly Gln Ala Asp Leu Asn Lys Asn Glu
          50          55          60

cca tgg gat cta cca aag att gca aag atg ggg gag aag gag ttt tac      422
Pro Trp Asp Leu Pro Lys Ile Ala Lys Met Gly Glu Lys Glu Phe Tyr
    65          70          75

ttt ttc tgc cag agg gat ccg aag tat ccg acc ggg atg agg acg aac      470
Phe Phe Cys Gln Arg Asp Arg Lys Tyr Pro Thr Gly Met Arg Thr Asn
    80          85          90

cgt gcg acc gtg tct ggt tat tgg aag gcg acc ggg aag gac aag gag      518
Arg Ala Thr Val Ser Gly Tyr Trp Lys Ala Thr Gly Lys Asp Lys Glu
    95          100          105

atc ttt aga ggc aaa ggt tgt ctt gtt ggg atg aag aaa aca ctt gtt      566
Ile Phe Arg Gly Lys Gly Cys Leu Val Gly Met Lys Lys Thr Leu Val
    110          115          120          125

ttc tat aca gga aga gct cct aaa ggt gaa aag acc aat tgg gtt atg      614
Phe Tyr Thr Gly Arg Ala Pro Lys Gly Glu Lys Thr Asn Trp Val Met
          130          135          140

cat gaa tat cgt ctt gat gga aaa tat tct tat cat aac ctc ccc aaa      662
His Glu Tyr Arg Leu Asp Gly Lys Tyr Ser Tyr His Asn Leu Pro Lys
          145          150          155

acc gca agg gat gaa tgg gtg gtg tgt agg gtt ttt cac aag aac gct      710
Thr Ala Arg Asp Glu Trp Val Val Cys Arg Val Phe His Lys Asn Ala
          160          165          170

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Pro Ser Thr Thr Ile Thr Thr Thr Lys Gln Leu Ser Arg Ile Asp Ser
          175          180          185

ctt gat aac att gat cat ctc tta gac ttc tca tct ctc cct cct ctc      806
Leu Asp Asn Ile Asp His Leu Leu Asp Phe Ser Ser Leu Pro Pro Leu
    190          195          200          205

ata gat ccg ggt ttc ttg ggt caa ccc gcc caa gct tct ccg gtg ccc      854
Ile Asp Pro Gly Phe Leu Gly Gln Pro Ala Gln Ala Ser Pro Val Pro
          210          215          220

gtc aac aac acg atc tca aac ctg tct cca cca tcc tac aac cgc acc      902
Val Asn Asn Thr Ile Ser Asn Leu Ser Pro Pro Ser Tyr Asn Arg Thr
          225          230          235

agt cga caa cac tta cct tcc tac cca agc tct caa ttt ccc tta cca      950

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MBI16 Sequence Listing.ST25

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 Leu Gly Pro
 255

aataacaaag gtatgatcaa gttggagcat tctcttgatga gtgtgtctca agaaaccggt 1062
 ttgagttccg atgtgaacac aaccgcaacg ccagagatat cttcttatcc aatgatgatg 1122
 aatccggcaa tgatggatgg tagcaagtca gcgtgtgatg gtcttgatga cttgatcttc 1182
 tgggaagatt tatatactag cttaaatttg gaaaagggtta tttgttaatt gtgattgaag 1242
 agtggcatat tgattactcg tctagtgttt ttaatcgtgt aattagttcg tatataatat 1302
 acatgtacat aagatcatta gggttattag gcattggact ttagttcggg gattgcttac 1362
 ctagttttta gcttgagaaa aaaggctgtc attgggggtta tgtttctttg tgattaactt 1422
 gtacatatat acattttaat taaacgtatg gtttaaatacg tttaaaaaaa aaaaaaa 1479

<210> 42
 <211> 256
 <212> PRT
 <213> Arabidopsis thaliana

<400> 42

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 1 5 10 15

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 20 25 30

Ile Ile Thr His Tyr Leu Lys Glu Lys Val Phe Asn Ile Arg Phe Thr
 35 40 45

Ala Ala Ala Ile Gly Gln Ala Asp Leu Asn Lys Asn Glu Pro Trp Asp
 50 55 60

Leu Pro Lys Ile Ala Lys Met Gly Glu Lys Glu Phe Tyr Phe Phe Cys
 65 70 75 80

Gln Arg Asp Arg Lys Tyr Pro Thr Gly Met Arg Thr Asn Arg Ala Thr
 85 90 95

Val Ser Gly Tyr Trp Lys Ala Thr Gly Lys Asp Lys Glu Ile Phe Arg
 100 105 110

Gly Lys Gly Cys Leu Val Gly Met Lys Lys Thr Leu Val Phe Tyr Thr
 115 120 125

Gly Arg Ala Pro Lys Gly Glu Lys Thr Asn Trp Val Met His Glu Tyr
 130 135 140

Arg Leu Asp Gly Lys Tyr Ser Tyr His Asn Leu Pro Lys Thr Ala Arg
 145 150 155 160

Asp Glu Trp Val Val Cys Arg Val Phe His Lys Asn Ala Pro Ser Thr
 165 170 175

MBI16 Sequence Listing.ST25

Thr Ile Thr Thr Thr Lys Gln Leu Ser Arg Ile Asp Ser Leu Asp Asn
180 185 190

Ile Asp His Leu Leu Asp Phe Ser Ser Leu Pro Pro Leu Ile Asp Pro
195 200 205

Gly Phe Leu Gly Gln Pro Ala Gln Ala Ser Pro Val Pro Val Asn Asn
210 215 220

Thr Ile Ser Asn Leu Ser Pro Pro Ser Tyr Asn Arg Thr Ser Arg Gln
225 230 235 240

His Leu Pro Ser Tyr Pro Ser Ser Gln Phe Pro Leu Pro Leu Gly Pro
245 250 255

<210> 43
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<212> DNA
<213> Arabidopsis thaliana

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<222> (1) .. (825)
<223> G197

<400> 43
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Trp Thr Lys Glu Glu Asp Asp Lys Leu Ile Ser Tyr Ile Lys Ala His
20 25 30
ggg gaa ggt tgt tgg cgt tct ctt cct aga tcc gcc ggt ctt caa cgt 144
Gly Glu Gly Cys Trp Arg Ser Leu Pro Arg Ser Ala Gly Leu Gln Arg
35 40 45
tgc gga aaa agc tgt cgt ctc cga tgg att aac tat ctc cga cct gat 192
Cys Gly Lys Ser Cys Arg Leu Arg Trp Ile Asn Tyr Leu Arg Pro Asp
50 55 60
ctc aag agg ggt aac ttc acc ctc gaa gaa gat gat ctc atc atc aaa 240
Leu Lys Arg Gly Asn Phe Thr Leu Glu Glu Asp Asp Leu Ile Ile Lys
65 70 75 80
cta cat agc ctt ctc ggt aac aag tgg tct ctt att gcg acg aga tta 288
Leu His Ser Leu Leu Gly Asn Lys Trp Ser Leu Ile Ala Thr Arg Leu
85 90 95
cca gga aga aca gat aac gag att aag aat tac tgg aac aca cat gtt 336
Pro Gly Arg Thr Asp Asn Glu Ile Lys Asn Tyr Trp Asn Thr His Val
100 105 110
aag agg aag cta tta aga aaa ggg att gat ccg gcg act cat cga cct 384
Lys Arg Lys Leu Leu Arg Lys Gly Ile Asp Pro Ala Thr His Arg Pro
115 120 125
atc aac gag acc aaa act tct caa gat tcg tct gat tct agt aaa aca 432
Ile Asn Glu Thr Lys Thr Ser Gln Asp Ser Ser Asp Ser Ser Lys Thr
130 135 140
gag gac cct ctt gtc aag att ctc tct ttt ggt cct cag ctg gag aaa 480
Glu Asp Pro Leu Val Lys Ile Leu Ser Phe Gly Pro Gln Leu Glu Lys
145 150 155 160
ata gca aat ttc ggg gac gag aga att caa aag aga gtt gag tac tca 528
Ile Ala Asn Phe Gly Asp Glu Arg Ile Gln Lys Arg Val Glu Tyr Ser
165 170 175

MBI16 Sequence Listing.ST25

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gtt gtt gaa gaa aga tgt ctg gac ttg aat ctt gag ctt agg atc agt      576
Val Val Glu Glu Arg Cys Leu Asp Leu Asn Leu Glu Leu Arg Ile Ser
      180      185      190

cca cca tgg caa gac aag ctc cat gat gag agg aac cta agg ttt ggg      624
Pro Pro Trp Gln Asp Lys Leu His Asp Glu Arg Asn Leu Arg Phe Gly
      195      200      205

aga gtg aag tat agg tgc agt gcg tgc cgt ttt gga ttc ggg aac ggc      672
Arg Val Lys Tyr Arg Cys Ser Ala Cys Arg Phe Gly Phe Gly Asn Gly
      210      215      220

aag gag tgt agc tgt aat aat gtg aaa tgt caa aca gag gac agt agt      720
Lys Glu Cys Ser Cys Asn Asn Val Lys Cys Gln Thr Glu Asp Ser Ser
      225      230      235

agc agc agt tat tct tca acc gac att agt agt agc att ggt tat gac      768
Ser Ser Ser Tyr Ser Ser Thr Asp Ile Ser Ser Ser Ile Gly Tyr Asp
      245      250      255

ttc ttg ggt cta aac aac act agg gtt ttg gat ttt agc act ttg gaa      816
Phe Leu Gly Leu Asn Asn Thr Arg Val Leu Asp Phe Ser Thr Leu Glu
      260      265      270

atg aaa tga
Met Lys
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<210> 44
<211> 274
<212> PRT
<213> Arabidopsis thaliana

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<400> 44

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Trp Thr Lys Glu Glu Asp Asp Lys Leu Ile Ser Tyr Ile Lys Ala His
20     25     30

Gly Glu Gly Cys Trp Arg Ser Leu Pro Arg Ser Ala Gly Leu Gln Arg
35     40     45

Cys Gly Lys Ser Cys Arg Leu Arg Trp Ile Asn Tyr Leu Arg Pro Asp
50     55     60

Leu Lys Arg Gly Asn Phe Thr Leu Glu Glu Asp Asp Leu Ile Ile Lys
65     70     75     80

Leu His Ser Leu Leu Gly Asn Lys Trp Ser Leu Ile Ala Thr Arg Leu
85     90     95

Pro Gly Arg Thr Asp Asn Glu Ile Lys Asn Tyr Trp Asn Thr His Val
100    105    110

Lys Arg Lys Leu Leu Arg Lys Gly Ile Asp Pro Ala Thr His Arg Pro
115    120    125

Ile Asn Glu Thr Lys Thr Ser Gln Asp Ser Ser Asp Ser Ser Lys Thr
130    135    140

Glu Asp Pro Leu Val Lys Ile Leu Ser Phe Gly Pro Gln Leu Glu Lys
145    150    155    160

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MBI16 Sequence Listing.ST25

Ile Ala Asn Phe Gly Asp Glu Arg Ile Gln Lys Arg Val Glu Tyr Ser
 165 170 175

Val Val Glu Glu Arg Cys Leu Asp Leu Asn Leu Glu Leu Arg Ile Ser
 180 185 190

Pro Pro Trp Gln Asp Lys Leu His Asp Glu Arg Asn Leu Arg Phe Gly
 195 200 205

Arg Val Lys Tyr Arg Cys Ser Ala Cys Arg Phe Gly Phe Gly Asn Gly
 210 215 220

Lys Glu Cys Ser Cys Asn Asn Val Lys Cys Gln Thr Glu Asp Ser Ser
 225 230 240

Ser Ser Ser Tyr Ser Ser Thr Asp Ile Ser Ser Ser Ile Gly Tyr Asp
 245 250 255

Phe Leu Gly Leu Asn Asn Thr Arg Val Leu Asp Phe Ser Thr Leu Glu
 260 265 270

Met Lys

<210> 45
 <211> 918
 <212> DNA
 <213> Arabidopsis thalina

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 <222> (30)..(839)
 <223> G255

<400> 45
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 1 5

aaa gaa cac atg aac aaa ggt gct tgg act aaa gaa gaa gat gag aga 101
 Lys Glu His Met Asn Lys Gly Ala Trp Thr Lys Glu Glu Asp Glu Arg
 10 15 20

cta gtc tct tac atc aag tct cac ggt gaa ggt tgt tgg cga tct ctt 149
 Leu Val Ser Tyr Ile Lys Ser His Gly Glu Gly Cys Trp Arg Ser Leu
 25 30 35 40

cct aga gcc gct ggt ctc ctt cgc tgc ggt aaa agc tgc cgt ctt cgg 197
 Pro Arg Ala Ala Gly Leu Leu Arg Cys Gly Lys Ser Cys Arg Leu Arg
 45 50 55

tgg att aac tat ctc cga cct gat ctc aaa aga gga aac ttt aca cat 245
 Trp Ile Asn Tyr Leu Arg Pro Asp Leu Lys Arg Gly Asn Phe Thr His
 60 65 70

gat gaa gat gaa ctt atc atc aag ctt cat agc ctc cta ggc aac aag 293
 Asp Glu Asp Glu Leu Ile Ile Lys Leu His Ser Leu Leu Gly Asn Lys
 75 80 85

tgg tct ttg att gcg gcg aga tta cct gga aga aca gat aac gag atc 341
 Trp Ser Leu Ile Ala Ala Arg Leu Pro Gly Arg Thr Asp Asn Glu Ile
 90 95 100

aag aac tac tgg aac aca cat ata aag agg aag ctt ttg agc aaa ggg 389

MBI16 Sequence Listing.ST25

Lys Asn Tyr Trp Asn Thr His Ile Lys Arg Lys Leu Leu Ser Lys Gly
 105 110 115 120
 att gat cca gcc act cat aga ggg atc aac gag gca aaa att tct gat 437
 Ile Asp Pro Ala Thr His Arg Gly Ile Asn Glu Ala Lys Ile Ser Asp
 125 130 135
 ttg aag aaa aca aag gac caa att gta aaa gat gtt tct ttt gtg aca 485
 Leu Lys Lys Thr Lys Asp Gln Ile Val Lys Asp Val Ser Phe Val Thr
 140 145 150
 aag ttt gag gaa aca gac aag tct ggg gac cag aag caa aat aag tat 533
 Lys Phe Glu Glu Thr Asp Lys Ser Gly Asp Gln Lys Gln Asn Lys Tyr
 155 160 165
 att cga aat ggg tta gtt tgc aaa gaa gag aga gtt gtt gtt gaa gaa 581
 Ile Arg Asn Gly Leu Val Cys Lys Glu Glu Arg Val Val Val Glu Glu
 170 175 180
 aaa ata ggc cca gat ttg aat ctt gag ctt agg atc agt cca cca tgg 629
 Lys Ile Gly Pro Asp Leu Asn Leu Glu Leu Arg Ile Ser Pro Pro Trp
 185 190 195 200
 caa aac cag aga gaa ata tct act tgc act gcg tcc cgt ttt tac atg 677
 Gln Asn Gln Arg Glu Ile Ser Thr Cys Thr Ala Ser Arg Phe Tyr Met
 205 210 215
 gaa aac gac atg gag tgt agt agt gaa act gtg aaa tgt caa aca gag 725
 Glu Asn Asp Met Glu Cys Ser Ser Glu Thr Val Lys Cys Gln Thr Glu
 220 225 230
 aat agt agc agc att agc tat tct tct att gat att agt agt agt aac 773
 Asn Ser Ser Ser Ile Ser Tyr Ser Ser Ile Asp Ile Ser Ser Ser Asn
 235 240 245
 gtt ggt tat gac ttc ttg ggt ttg aag aca aga att ttg gat ttt cga 821
 Val Gly Tyr Asp Phe Leu Gly Leu Lys Thr Arg Ile Leu Asp Phe Arg
 250 255 260
 agc ttg gaa atg aaa taa atgaatagta ttagattctt aatttgtagg 869
 Ser Leu Glu Met Lys
 265
 tctgataatg aatgtagat tcgcggccct ctgacaggc ctcgtaccg 918

<210> 46
 <211> 269
 <212> PRT
 <213> Arabidopsis thalina

<400> 46

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 Trp Thr Lys Glu Glu Asp Glu Arg Leu Val Ser Tyr Ile Lys Ser His
 20 25 30
 Gly Glu Gly Cys Trp Arg Ser Leu Pro Arg Ala Ala Gly Leu Leu Arg
 35 40 45
 Cys Gly Lys Ser Cys Arg Leu Arg Trp Ile Asn Tyr Leu Arg Pro Asp
 50 55 60
 Leu Lys Arg Gly Asn Phe Thr His Asp Glu Asp Glu Leu Ile Ile Lys
 65 70 75 80
 Leu His Ser Leu Leu Gly Asn Lys Trp Ser Leu Ile Ala Ala Arg Leu
 85 90 95

MBI16 Sequence Listing.ST25

Pro Gly Arg Thr Asp Asn Glu Ile Lys Asn Tyr Trp Asn Thr His Ile
 100 105 110

Lys Arg Lys Leu Leu Ser Lys Gly Ile Asp Pro Ala Thr His Arg Gly
 115 120 125

Ile Asn Glu Ala Lys Ile Ser Asp Leu Lys Lys Thr Lys Asp Gln Ile
 130 135 140

Val Lys Asp Val Ser Phe Val Thr Lys Phe Glu Glu Thr Asp Lys Ser
 145 150 155 160

Gly Asp Gln Lys Gln Asn Lys Tyr Ile Arg Asn Gly Leu Val Cys Lys
 165 170 175

Glu Glu Arg Val Val Val Glu Glu Lys Ile Gly Pro Asp Leu Asn Leu
 180 185 190

Glu Leu Arg Ile Ser Pro Pro Trp Gln Asn Gln Arg Glu Ile Ser Thr
 195 200 205

Cys Thr Ala Ser Arg Phe Tyr Met Glu Asn Asp Met Glu Cys Ser Ser
 210 215 220

Glu Thr Val Lys Cys Gln Thr Glu Asn Ser Ser Ser Ile Ser Tyr Ser
 225 230 235 240

Ser Ile Asp Ile Ser Ser Ser Asn Val Gly Tyr Asp Phe Leu Gly Leu
 245 250 255

Lys Thr Arg Ile Leu Asp Phe Arg Ser Leu Glu Met Lys
 260 265

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 <223> G1113

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 Pro Thr Asp Phe Lys Glu Leu Gln Ile Pro Gly Tyr Val Leu Lys Thr
 5 10 15

ctt tac gtc atc ggt ttc ttt aga gac atg gtc gat gct ctt tgt cct 152
 Leu Tyr Val Ile Gly Phe Phe Arg Asp Met Val Asp Ala Leu Cys Pro
 20 25 30 35

tac atc ggt cta cca agt ttt ctt gac cac aac gag acc tct cga tcc 200
 Tyr Ile Gly Leu Pro Ser Phe Leu Asp His Asn Glu Thr Ser Arg Ser
 40 45 50

gac ccg acc cga ctc gct ctc tcc acg tca gca act ctt gcc aac gag 248

MBI16 Sequence Listing.ST25

Asp	Pro	Thr	Arg	Leu	Ala	Leu	Ser	Thr	Ser	Ala	Thr	Leu	Ala	Asn	Glu		
			55				60						65				
tta	atc	ccg	gtg	ggt	cgt	ttc	tcc	gat	ctt	tta	acc	gat	ccg	gaa	gat	296	
Leu	Ile	Pro	Val	Val	Arg	Phe	Ser	Asp	Leu	Leu	Thr	Asp	Pro	Glu	Asp		
		70					75					80					
tgc	tgc	acg	gtt	tgc	tta	tcc	gat	ttt	gta	tcc	gac	gat	aag	att	aga	344	
Cys	Cys	Thr	Val	Cys	Leu	Ser	Asp	Phe	Val	Ser	Asp	Asp	Lys	Ile	Arg		
		85				90					95						
cag	ctg	ccg	aag	tgt	gga	cac	gtg	ttt	cat	cat	cgt	tgt	tta	gac	cgt	392	
Gln	Leu	Pro	Lys	Cys	Gly	His	Val	Phe	His	His	Arg	Cys	Leu	Asp	Arg		
100					105				110						115		
tgg	atc	gtt	gac	tgt	aat	aag	ata	acg	tgc	ccg	att	tgt	cgg	aac	cgg	440	
Trp	Ile	Val	Asp	Cys	Asn	Lys	Ile	Thr	Cys	Pro	Ile	Cys	Arg	Asn	Arg		
				120					125					130			
ttc	tta	ccg	gag	gaa	aag	tcc	acg	ccg	ttt	gat	tgg	ggg	act	tca	gat	488	
Phe	Leu	Pro	Glu	Glu	Lys	Ser	Thr	Pro	Phe	Asp	Trp	Gly	Thr	Ser	Asp		
			135					140					145				
tgg	ttt	aga	gat	gaa	gtg	gag	agt	acc	aac	taa	taatgatggg	tttactttta				541	
Trp	Phe	Arg	Asp	Glu	Val	Glu	Ser	Thr	Asn								
		150					155										
ctttttacttt	ttttcacggg	aatattttttc	tactgtataa	ttctttcttc	caaactactg											601	
tataattcaa	gtataagatt	atgtaattgt	gtatattagc	atcaatcatc	tttctttgt											660	

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 <211> 157
 <212> PRT
 <213> Arabidopsis thaliana
 <400> 48

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Leu	Lys	Thr	Leu	Tyr	Val	Ile	Gly	Phe	Phe	Arg	Asp	Met	Val	Asp	Ala
			20					25					30		
Leu	Cys	Pro	Tyr	Ile	Gly	Leu	Pro	Ser	Phe	Leu	Asp	His	Asn	Glu	Thr
		35					40					45			
Ser	Arg	Ser	Asp	Pro	Thr	Arg	Leu	Ala	Leu	Ser	Thr	Ser	Ala	Thr	Leu
	50					55				60					
Ala	Asn	Glu	Leu	Ile	Pro	Val	Val	Arg	Phe	Ser	Asp	Leu	Leu	Thr	Asp
65					70				75					80	
Pro	Glu	Asp	Cys	Cys	Thr	Val	Cys	Leu	Ser	Asp	Phe	Val	Ser	Asp	Asp
			85					90					95		
Lys	Ile	Arg	Gln	Leu	Pro	Lys	Cys	Gly	His	Val	Phe	His	His	Arg	Cys
			100					105					110		
Leu	Asp	Arg	Trp	Ile	Val	Asp	Cys	Asn	Lys	Ile	Thr	Cys	Pro	Ile	Cys
		115					120					125			
Arg	Asn	Arg	Phe	Leu	Pro	Glu	Glu	Lys	Ser	Thr	Pro	Phe	Asp	Trp	Gly
	130					135					140				

MBI16 Sequence Listing.ST25

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145 150 155

<210> 49
<211> 1201
<212> DNA
<213> Arabidopsis thaliana

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<222> (148) .. (996)
<223> G398

<400> 49
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cagcttttaga tcaaggtttt tctagtcctc tctactcata aagatcaaag cttttgctat 120
tctcattttc taccaagaga caatatc atg atg atg ggt aaa gag gat ttg ggt 174
Met Met Met Gly Lys Glu Asp Leu Gly
1 5

tta agt ctt agc ttg gga ttt gca caa aac cat cct ctc cag cta aat 222
Leu Ser Leu Ser Leu Gly Phe Ala Gln Asn His Pro Leu Gln Leu Asn
10 15 20 25

ctt aaa ccc act tct tca cca atg tcc aat ctc cag atg ttt cca tgg 270
Leu Lys Pro Thr Ser Ser Pro Met Ser Asn Leu Gln Met Phe Pro Trp
30 35 40

aac caa acc ctt gtt tct tcc tca gat caa caa aag caa cag ttt ctt 318
Asn Gln Thr Leu Val Ser Ser Ser Asp Gln Gln Lys Gln Gln Phe Leu
45 50 55

agg aaa atc gac gtg aac agc ttg cca aca acg gtg gat ttg gaa gag 366
Arg Lys Ile Asp Val Asn Ser Leu Pro Thr Thr Val Asp Leu Glu Glu
60 65 70

gag aca gga gtt tcg tct cca aac agt acg atc tcg agc aca gtg agt 414
Glu Thr Gly Val Ser Ser Pro Asn Ser Thr Ile Ser Ser Thr Val Ser
75 80 85

gga aag agg agg agt act gaa aga gaa ggt acc tcc ggt ggt ggt tgc 462
Gly Lys Arg Arg Ser Thr Glu Arg Glu Gly Thr Ser Gly Gly Gly Cys
90 95 100 105

gga gat gac ctt gac atc act cta gat aga tct tcc tca cgt gga acc 510
Gly Asp Asp Leu Asp Ile Thr Leu Asp Arg Ser Ser Ser Arg Gly Thr
110 115 120

tcc gat gaa gag gaa gat tac gga ggt gag act tgt agg aag aag ctt 558
Ser Asp Glu Glu Glu Asp Tyr Gly Gly Glu Thr Cys Arg Lys Lys Leu
125 130 135

aga cta tcc aaa gat caa tcc gca gtt ctc gaa gac act ttc aaa gag 606
Arg Leu Ser Lys Asp Gln Ser Ala Val Leu Glu Asp Thr Phe Lys Glu
140 145 150

cac aat act ctc aat ccc aaa cag aag ctg gct ttg gct aag aag cta 654
His Asn Thr Leu Asn Pro Lys Gln Lys Leu Ala Leu Ala Lys Lys Leu
155 160 165

ggt tta aca gca aga caa gtg gaa gtg tgg ttc caa aac aga aga gca 702
Gly Leu Thr Ala Arg Gln Val Glu Val Trp Phe Gln Asn Arg Arg Ala
170 175 180 185

agg aca aag tta aag cag acc gaa gtg gat tgc gag tat ttg aaa aga 750
Arg Thr Lys Leu Lys Gln Thr Glu Val Asp Cys Glu Tyr Leu Lys Arg
190 195 200

tgt gtt gag aaa tta acg gaa gag aat cgg cgg ctc gag aaa gag gca 798
Cys Val Glu Lys Leu Thr Glu Glu Asn Arg Arg Leu Glu Lys Glu Ala
205 210 215

MBI16 Sequence Listing.ST25

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gcg gaa cta aga gca tta aag ctt tca ccg cgg ttg tat ggt cag atg      846
Ala Glu Leu Arg Ala Leu Lys Leu Ser Pro Arg Leu Tyr Gly Gln Met
      220                      225                      230

agt cca ccg acc aca ctt ttg atg tgt cca tcg tgt gaa cgt gtg gcc      894
Ser Pro Pro Thr Thr Leu Leu Met Cys Pro Ser Cys Glu Arg Val Ala
      235                      240                      245

gga cca tcc tca tct aac cac aac cag cga tct gtc tca ttg agt cca      942
Gly Pro Ser Ser Ser Asn His Asn Gln Arg Ser Val Ser Leu Ser Pro
      250                      255                      260                      265

tgg ctc caa atg gcc cat ggg tca acc ttt gat gtg atg cgt cct agg      990
Trp Leu Gln Met Ala His Gly Ser Thr Phe Asp Val Met Arg Pro Arg
      270                      275                      280

tct taa ctttaatgct gcttctatgg gttgtgtgtg ggtcattgta ctttttagat      1046
Ser

tattgactct cagctaattgt atccttaaaa gcctttttct actttttaa at ttactttaat      1106

ctaattaaat tagttgtcca tgtcttcttg ataacaaaaa aatttataat tataaaaaaa      1166

aaaaacagga taaaaaaaaa aaaaaaaaaa aaaaaa                                1201

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<211> 282
<212> PRT
<213> Arabidopsis thaliana

<400> 50

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20                      25                      30

Met Ser Asn Leu Gln Met Phe Pro Trp Asn Gln Thr Leu Val Ser Ser
35                      40                      45

Ser Asp Gln Gln Lys Gln Gln Phe Leu Arg Lys Ile Asp Val Asn Ser
50                      55                      60

Leu Pro Thr Thr Val Asp Leu Glu Glu Glu Thr Gly Val Ser Ser Pro
65                      70                      75                      80

Asn Ser Thr Ile Ser Ser Thr Val Ser Gly Lys Arg Arg Ser Thr Glu
85                      90                      95

Arg Glu Gly Thr Ser Gly Gly Gly Cys Gly Asp Asp Leu Asp Ile Thr
100                      105                      110

Leu Asp Arg Ser Ser Ser Arg Gly Thr Ser Asp Glu Glu Glu Asp Tyr
115                      120                      125

Gly Gly Glu Thr Cys Arg Lys Lys Leu Arg Leu Ser Lys Asp Gln Ser
130                      135                      140

Ala Val Leu Glu Asp Thr Phe Lys Glu His Asn Thr Leu Asn Pro Lys
145                      150                      155                      160

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MBI16 Sequence Listing.ST25

Gln Lys Leu Ala Leu Ala Lys Lys Leu Gly Leu Thr Ala Arg Gln Val
165 170 175

Glu Val Trp Phe Gln Asn Arg Arg Ala Arg Thr Lys Leu Lys Gln Thr
180 185 190

Glu Val Asp Cys Glu Tyr Leu Lys Arg Cys Val Glu Lys Leu Thr Glu
195 200 205

Glu Asn Arg Arg Leu Glu Lys Glu Ala Ala Glu Leu Arg Ala Leu Lys
210 215 220

Leu Ser Pro Arg Leu Tyr Gly Gln Met Ser Pro Pro Thr Thr Leu Leu
225 230 235 240

Met Cys Pro Ser Cys Glu Arg Val Ala Gly Pro Ser Ser Ser Asn His
245 250 255

Asn Gln Arg Ser Val Ser Leu Ser Pro Trp Leu Gln Met Ala His Gly
260 265 270

Ser Thr Phe Asp Val Met Arg Pro Arg Ser
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<222> (120)..(797)
<223> G395

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gagaggacac gctgacaagc tgactctagc agatctggta ccgtcgacaa ggaggaaga 119
atg ccc tta gga gca gct acg gtt gtg gag gag gaa gag gag gag gag 167
Met Pro Leu Gly Ala Ala Thr Val Val Glu Glu Glu Glu Glu Glu
1 5 10 15
gaa gcg gtg cct agt atg tca gta tcg ccg ccg gat agt gta acg tcg 215
Glu Ala Val Pro Ser Met Ser Val Ser Pro Pro Asp Ser Val Thr Ser
20 25 30
tcg ttt caa ttg gac ttt ggg att aaa agt tat ggt tat gag aga aga 263
Ser Phe Gln Leu Asp Phe Gly Ile Lys Ser Tyr Gly Tyr Glu Arg Arg
35 40 45
agc aat aag aga gat att gat gat gaa gtg gag aga tca gcc tca aga 311
Ser Asn Lys Arg Asp Ile Asp Asp Glu Val Glu Arg Ser Ala Ser Arg
50 55 60
gcc agc aac gaa gac aac gat gac gag aat gga tcc act agg aag aaa 359
Ala Ser Asn Glu Asp Asn Asp Asp Glu Asn Gly Ser Thr Arg Lys Lys
65 70 75 80
ctt aga ctc tcc aaa gac caa tct gct ttt ctt gaa gac agc ttc aaa 407
Leu Arg Leu Ser Lys Asp Gln Ser Ala Phe Leu Glu Asp Ser Phe Lys
85 90 95
gaa cac agt acc ctt aat cct aaa cag aag att gca ttg gcg aag cag 455
Glu His Ser Thr Leu Asn Pro Lys Gln Lys Ile Ala Leu Ala Lys Gln
100 105 110

MBI16 Sequence Listing.ST25

ttg aat ctt cgt cct cgt cag gtt gaa gtc tgg ttt caa aac aga cga 503
 Leu Asn Leu Arg Pro Arg Gln Val Glu Val Trp Phe Gln Asn Arg Arg
 115 120 125

gcc agg aca aag ctg aag caa acg gaa gtg gac tgt gaa tac cta aag 551
 Ala Arg Thr Lys Leu Lys Gln Thr Glu Val Asp Cys Glu Tyr Leu Lys
 130 135 140

aga tgc tgt gag tca cta acc gaa gaa aac cgg agg ctt caa aaa gag 599
 Arg Cys Cys Glu Ser Leu Thr Glu Glu Asn Arg Arg Leu Gln Lys Glu
 145 150 155 160

gtt aaa gaa ttg aga acc ttg aag act tcc aca ccc ttt tac atg caa 647
 Val Lys Glu Leu Arg Thr Leu Lys Thr Ser Thr Pro Phe Tyr Met Gln
 165 170 175

ctt ccg gcc act act ctc act atg tgc cct tct tgt gaa cgt gtt gcc 695
 Leu Pro Ala Thr Thr Leu Thr Met Cys Pro Ser Cys Glu Arg Val Ala
 180 185 190

act tca gca gca cag ccc tcc acg tca gct gcc cac aac ctc tgt ttg 743
 Thr Ser Ala Ala Gln Pro Ser Thr Ser Ala Ala His Asn Leu Cys Leu
 195 200 205

tcc acg tca tca ttg att ccg gtt aag cct cgg ccg gcc aaa caa gtt 791
 Ser Thr Ser Ser Leu Ile Pro Val Lys Pro Arg Pro Ala Lys Gln Val
 210 215 220

tca tga aagcacctgc gaaatacagt ttgagcaaac gggcggccgc tctagacagg 847
 Ser
 225

cctcgtaccg gatcctctag ctagagcttt cgttcgtatc atcgggtttcg acaacggtcg 907
 tcaagttcaa tgacatcagt ttgattgcgc 937

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 <213> Arabidopsis thaliana

<400> 52

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 20 25 30

Ser Phe Gln Leu Asp Phe Gly Ile Lys Ser Tyr Gly Tyr Glu Arg Arg
 35 40 45

Ser Asn Lys Arg Asp Ile Asp Asp Glu Val Glu Arg Ser Ala Ser Arg
 50 55 60

Ala Ser Asn Glu Asp Asn Asp Asp Glu Asn Gly Ser Thr Arg Lys Lys
 65 70 75 80

Leu Arg Leu Ser Lys Asp Gln Ser Ala Phe Leu Glu Asp Ser Phe Lys
 85 90 95

Glu His Ser Thr Leu Asn Pro Lys Gln Lys Ile Ala Leu Ala Lys Gln
 100 105 110

Leu Asn Leu Arg Pro Arg Gln Val Glu Val Trp Phe Gln Asn Arg Arg
 115 120 125

MBI16 Sequence Listing.ST25

Ala Arg Thr Lys Leu Lys Gln Thr Glu Val Asp Cys Glu Tyr Leu Lys
130 135 140

Arg Cys Cys Glu Ser Leu Thr Glu Glu Asn Arg Arg Leu Gln Lys Glu
145 150 155 160

Val Lys Glu Leu Arg Thr Leu Lys Thr Ser Thr Pro Phe Tyr Met Gln
165 170 175

Leu Pro Ala Thr Thr Leu Thr Met Cys Pro Ser Cys Glu Arg Val Ala
180 185 190

Thr Ser Ala Ala Gln Pro Ser Thr Ser Ala Ala His Asn Leu Cys Leu
195 200 205

Ser Thr Ser Ser Leu Ile Pro Val Lys Pro Arg Pro Ala Lys Gln Val
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Ser
225

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<400> 53
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Met Gly Phe Asp Asp Thr
1 5

tgc aac aca ggt ctt gtt ctt gga tta ggt ccc tca cca att tca aat 102
Cys Asn Thr Gly Leu Val Leu Gly Leu Gly Pro Ser Pro Ile Ser Asn
10 15 20

aat tac aat agt acc atc aga caa tcc tcc gtt tac aag ctc gag ccg 150
Asn Tyr Asn Ser Thr Ile Arg Gln Ser Ser Val Tyr Lys Leu Glu Pro
25 30 35

tcg ttg act cta tgc ctc tcg ggc gat ccc tcg gtt acc gtg gtg acc 198
Ser Leu Thr Leu Cys Leu Ser Gly Asp Pro Ser Val Thr Val Val Thr
40 45 50

gga gct gac cag cta tgc cgt cag acg tca tct cac agc gga gtc tct 246
Gly Ala Asp Gln Leu Cys Arg Gln Thr Ser Ser His Ser Gly Val Ser
55 60 65 70

tct ttc tca agc ggg agg gtg gtg aaa aga gag aga gac ggt ggc gaa 294
Ser Phe Ser Ser Gly Arg Val Val Lys Arg Glu Arg Asp Gly Gly Glu
75 80 85

gag tcg ccg gag gag gaa gag atg acg gag aga gtt ata agt gat tac 342
Glu Ser Pro Glu Glu Glu Met Thr Glu Arg Val Ile Ser Asp Tyr
90 95 100

cat gaa gat gaa gaa ggt att agt gct aga aaa aaa ctt agg ctt acg 390
His Glu Asp Glu Glu Gly Ile Ser Ala Arg Lys Lys Leu Arg Leu Thr
105 110 115

aaa caa caa tct gct ctt ctt gag gaa agc ttc aag gat cat agc acc 438

MBI16 Sequence Listing.ST25

Lys	Gln	Gln	Ser	Ala	Leu	Leu	Glu	Glu	Ser	Phe	Lys	Asp	His	Ser	Thr		
120						125					130						
ctt	aat	ccc	aaa	caa	aag	caa	gtt	ctg	gct	aga	cag	ctg	aat	cta	agg		486
Leu	Asn	Pro	Lys	Gln	Lys	Gln	Val	Leu	Ala	Arg	Gln	Leu	Asn	Leu	Arg		
135					140					145					150		
cct	aga	caa	gtt	gaa	gta	tgg	ttt	caa	aat	aga	aga	gcc	agg	aca	aag		534
Pro	Arg	Gln	Val	Glu	Val	Trp	Phe	Gln	Asn	Arg	Arg	Ala	Arg	Thr	Lys		
				155					160					165			
ctg	aag	caa	aca	gaa	gta	gat	tgt	gag	ttt	ttg	aag	aag	tgt	tgt	gaa		582
Leu	Lys	Gln	Thr	Glu	Val	Asp	Cys	Glu	Phe	Leu	Lys	Lys	Cys	Cys	Glu		
			170				175						180				
aca	tta	gca	gat	gag	aac	ata	aga	ctt	cag	aaa	gag	att	caa	gaa	ctc		630
Thr	Leu	Ala	Asp	Glu	Asn	Ile	Arg	Leu	Gln	Lys	Glu	Ile	Gln	Glu	Leu		
		185					190					195					
aaa	acc	cta	aaa	ttg	act	cag	ccc	ttt	tac	atg	cac	atg	cct	gca	tcg		678
Lys	Thr	Leu	Lys	Leu	Thr	Gln	Pro	Phe	Tyr	Met	His	Met	Pro	Ala	Ser		
	200					205					210						
act	cta	acg	aag	tgt	cct	tct	tgt	gag	aga	atc	ggc	ggc	ggc	ggc	ggg		726
Thr	Leu	Thr	Lys	Cys	Pro	Ser	Cys	Glu	Arg	Ile	Gly	Gly	Gly	Gly	Gly		
	215				220				225						230		
ggg	aat	gga	gga	gga	ggg	ggc	ggc	agc	ggg	gct	acc	gcg	gtg	att	gta		774
Gly	Asn	Gly	Gly	Gly	Gly	Gly	Gly	Ser	Gly	Ala	Thr	Ala	Val	Ile	Val		
				235					240					245			
gat	gga	agt	acg	gcc	aaa	gga	gct	ttc	tct	atc	tcc	tca	aag	cct	cac		822
Asp	Gly	Ser	Thr	Ala	Lys	Gly	Ala	Phe	Ser	Ile	Ser	Ser	Lys	Pro	His		
			250					255					260				
ttc	ttc	aac	cct	ttt	act	aac	cca	tct	gca	gct	tgt	tga	atagttaatt				871
Phe	Phe	Asn	Pro	Phe	Thr	Asn	Pro	Ser	Ala	Ala	Cys						
		265					270										
cgtttaattt	tattacttaa	aatattaatt	ttcttttttt	ttttgggtgg	catttt												927

<210> 54
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Met	Gly	Phe	Asp	Asp	Thr	Cys	Asn	Thr	Gly	Leu	Val	Leu	Gly	Leu	Gly		
1				5					10					15			
Pro	Ser	Pro	Ile	Ser	Asn	Asn	Tyr	Asn	Ser	Thr	Ile	Arg	Gln	Ser	Ser		
			20					25					30				
Val	Tyr	Lys	Leu	Glu	Pro	Ser	Leu	Thr	Leu	Cys	Leu	Ser	Gly	Asp	Pro		
		35					40					45					
Ser	Val	Thr	Val	Val	Thr	Gly	Ala	Asp	Gln	Leu	Cys	Arg	Gln	Thr	Ser		
	50					55					60						
Ser	His	Ser	Gly	Val	Ser	Ser	Phe	Ser	Ser	Gly	Arg	Val	Val	Lys	Arg		
	65				70					75					80		
Glu	Arg	Asp	Gly	Gly	Glu	Glu	Ser	Pro	Glu	Glu	Glu	Glu	Met	Thr	Glu		
				85					90					95			
Arg	Val	Ile	Ser	Asp	Tyr	His	Glu	Asp	Glu	Glu	Gly	Ile	Ser	Ala	Arg		
			100					105					110				

MBI16 Sequence Listing.ST25

Lys Lys Leu Arg Leu Thr Lys Gln Gln Ser Ala Leu Leu Glu Glu Ser
 115 120 125
 Phe Lys Asp His Ser Thr Leu Asn Pro Lys Gln Lys Gln Val Leu Ala
 130 135 140
 Arg Gln Leu Asn Leu Arg Pro Arg Gln Val Glu Val Trp Phe Gln Asn
 145 150 155 160
 Arg Arg Ala Arg Thr Lys Leu Lys Gln Thr Glu Val Asp Cys Glu Phe
 165 170 175
 Leu Lys Lys Cys Cys Glu Thr Leu Ala Asp Glu Asn Ile Arg Leu Gln
 180 185 190
 Lys Glu Ile Gln Glu Leu Lys Thr Leu Lys Leu Thr Gln Pro Phe Tyr
 195 200 205
 Met His Met Pro Ala Ser Thr Leu Thr Lys Cys Pro Ser Cys Glu Arg
 210 215 220
 Ile Gly Gly Gly Gly Gly Gly Asn Gly Gly Gly Gly Gly Gly Ser Gly
 225 230 235 240
 Ala Thr Ala Val Ile Val Asp Gly Ser Thr Ala Lys Gly Ala Phe Ser
 245 250 255
 Ile Ser Ser Lys Pro His Phe Phe Asn Pro Phe Thr Asn Pro Ser Ala
 260 265 270
 Ala Cys

INTERNATIONAL SEARCH REPORT

In application No.

PCT/US00/31458

A. CLASSIFICATION OF SUBJECT MATTER

IPC(7) : C12N 5/04, 5/10, 15/00, 15/09, 15/63, 15/70, 15/74, 15/82, 15/87; C07H 21/02, 21/04; A01H 1/00, 9/00, 11/00
 US CL : 435/320.1, 419, 468; 536/23.1; 800/ 278, 295

B. FIELDS SEARCHED

Minimum documentation searched (classification system followed by classification symbols)
 U.S. : 435/320.1, 419, 468; 536/23.1; 800/ 278, 295

Documentation searched other than minimum documentation to the extent that such documents are included in the fields searched

Electronic data base consulted during the international search (name of data base and, where practicable, search terms used)
 Please See Continuation Sheet

C. DOCUMENTS CONSIDERED TO BE RELEVANT

Category *	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
P,X ---	Database GenEmbl on STIC, USPTO, (Arlington, VA, USA), GenBank Accession AC002388, LIN et al. 'Sequence analysis of chromosome 2 of the plant Arabidopsis thaliana,' abstract, Nature, 1999, Vol. 402, 761-768.	4-6 ----- 1-3, 7-13, 25-27
P,Y ---	Database EST on STIC, USPTO, (Arlington, VA, USA), GenBank Accession AV552445, ASAMIZU et al. 'A large scale analysis of cDNA in Arabidopsis thaliana: generation of 12,028 non-redundant expressed sequence tags from normalized and size-selected cDNA libraries,' abstract, DNA Research, 2000, Vol. 7, 175-180.	4-6 ----- 1-3, 7-13, 25-27
P,X ---	Database EST on STIC, USPTO, (Arlington, VA, USA), Genbank Accession AI997809, CHEN et al. unpublished, abstract, 08 September 1999.	4-6 ----- 1-3, 7-13, 25-27
X ---	Database EST on STIC, USPTO, (Arlington, VA, USA), GenBank Accession N97133, NEWMAN et al. 'Genes galore: a summary of methods for accessing results from large-scale partial sequencing of anonymous Arabidopsis cDNA clones,' abstract, Plant Physiology, 1994, Vol. 106, 1241-1255.	4-6 ----- 1-3, 7-13, 25-27
Y		

☒ Further documents are listed in the continuation of Box C.

☐ See patent family annex.

* Special categories of cited documents:	"T"	later document published after the international filing date or priority date and not in conflict with the application but cited to understand the principle or theory underlying the invention
"A" document defining the general state of the art which is not considered to be of particular relevance	"X"	document of particular relevance; the claimed invention cannot be considered novel or cannot be considered to involve an inventive step when the document is taken alone
"E" earlier application or patent published on or after the international filing date	"Y"	document of particular relevance; the claimed invention cannot be considered to involve an inventive step when the document is combined with one or more other such documents, such combination being obvious to a person skilled in the art
"L" document which may throw doubts on priority claim(s) or which is cited to establish the publication date of another citation or other special reason (as specified)	"&"	document member of the same patent family
"O" document referring to an oral disclosure, use, exhibition or other means		
"P" document published prior to the international filing date but later than the priority date claimed		

Date of the actual completion of the international search

13 February 2001 (13.02.2001)

Date of mailing of the international search report

07 MAR 2001

Name and mailing address of the ISA/US

Commissioner of Patents and Trademarks
 Box PCT
 Washington, D.C. 20231

Facsimile No. (703)305-3230

Authorized officer

Cynthia Collins

Telephone No. (703) 605-1210

INTERNATIONAL SEARCH REPORT

I. application No.

PCT/US00/31458

C (Continuation) DOCUMENTS CONSIDERED TO BE RELEVANT

Category*	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
X --- Y	Database EST on STIC, USPTO, (Arlington, VA, USA), GenBank Accession AA598183, NEWMAN et al. 'Geues galore: a summary of methods for accessing results from large-scale partial sequencing of anonymous Arabidopsis cDNA clones,' abstract. Plant Physiology, 1994, Vol. 106, 1241-1255.	4-6 ----- 1-3, 7-13, 25-27
X --- Y	Database PIR_66 on STIC, USPTO, (Arlington, VA, USA), Accession T00409, ROUNSLEY et al. unpublished, abstract, 01 February 1999.	11 ----- 1-10, 12-13, 25-27
X --- Y	Database SPTREMBL_15 on STIC, USPTO, (Arlington, VA, USA), Accession 022167, ROUNSLEY et al. unpublished, abstract, 01 January 1998.	11 ----- 1-10, 12-13, 25-27
T,E	RIECHMANN et al. Arabidopsis transcription factors: genome-wide comparative analysis among eukaryotes. Science. 15 December 2000, Vol. 290, pages 2105-2110.	
P,A	SUNG et al. Developmentally regulated expression of two MADS-box genes, MdMADS3 and MdMADS4, in the morphogenesis of flower buds and fruits in apple. Planta. March 2000, Vol. 210, pages 519-528.	
P,Y	RIECHMANN et al. A genomic perspective on plant transcription factors. Current Opinion in Plant Biology. October 2000, Vol. 3, pages 423-434, especially pages 427-428.	1-13, 25-27
Y	US 5,892,009 A (THOMASHOW et al.) 06 April 1999, column 14, lines 1-46.	1-3, 7-10, 12-13, 25-27
A	RATCLIFFE et al. Separation of shoot and floral identity in Arabidopsis. Development. March 1999, Vol. 126, pages 1109-1120.	
A	SUNG et al. Characterization of MdMADS2, a member of the SQUAMOSA subfamily of genes, in apple. Plant Physiology. August 1999, Vol. 120, pages 969-978.	
A	RIECHMANN et al. The AP2/EREBP family of plant transcription factors. Biol. Chem. June 1998, Vol. 379, pages 633-646.	
A	RIECHMANN et al. Determination of floral organ identity by Arabidopsis MADS domain homeotic proteins AP1, AP3, PI, and AG is independent of their DNA-binding specificity. Molecular Biology of the Cell. July 1997, Vol., pages 1243-1259.	
A	HEARD et al. Evolutionary diversity of symbiotically induced nodule MADS box genes: characterization of umhC5, a member of a novel subfamily. Molecular Plant-Microbe Interactions. July 1997, Vol. 10, No. 5, pages 665-676.	
A	RIECHMANN et al. MADS domain proteins in plant development. Biol. Chem. October 1997. Vol. 378, pages 1079-1101.	
A	RIECHMANN et al. DNA-binding properties of Arabidopsis MADS domain homeotic proteins APETALA1, APETALA3, PISTILLATA and AGAMOUS. Nucleic Acids Research. August 1996, Vol. 24, No. 16, pages 3134-3141.	
A	RIECHMANN et al. Dimerization specificity of Arabidopsis MADS domain homeotic proteins APETALA1, APETALA3, PISTILLATA, and AGAMOUS. Proc. Natl. Acad. Sci. USA. May 1996, Vol. 93, pages 4793-4798.	
A	HEARD et al. Symbiotic induction of a MADS-box gene during development of alfalfa root nodules. Proc. Natl. Acad. Sci. USA. June 1995, Vol. 92, pages 5273-5277.	

INTERNATIONAL SEARCH REPORT

International application No.

PCT/US00/31458

Box I Observations where certain claims were found unsearchable (Continuation of Item 1 of first sheet)

This international report has not been established in respect of certain claims under Article 17(2)(a) for the following reasons:

1. ☐ Claim Nos.:
because they relate to subject matter not required to be searched by this Authority, namely:
2. ☐ Claim Nos.:
because they relate to parts of the international application that do not comply with the prescribed requirements to such an extent that no meaningful international search can be carried out, specifically:
3. ☐ Claim Nos.:
because they are dependent claims and are not drafted in accordance with the second and third sentences of Rule 6.4(a).

Box II Observations where unity of invention is lacking (Continuation of Item 2 of first sheet)

This International Searching Authority found multiple inventions in this international application, as follows:
Please See Continuation Sheet

1. ☐ As all required additional search fees were timely paid by the applicant, this international search report covers all searchable claims.
2. ☐ As all searchable claims could be searched without effort justifying an additional fee, this Authority did not invite payment of any additional fee.
3. ☐ As only some of the required additional search fees were timely paid by the applicant, this international search report covers only those claims for which fees were paid, specifically claims Nos.:
4. ☒ No required additional search fees were timely paid by the applicant. Consequently, this international search report is restricted to the invention first mentioned in the claims; it is covered by claims Nos.: 1-13, 25-27 SEQ ID NOS:1 and 2

Remark on Protest

☐
☐

The additional search fees were accompanied by the applicant's protest.

No protest accompanied the payment of additional search fees.

INTERNATIONAL SEARCH REPORT

na application No.

PCT/US00/31458

BOX II. OBSERVATIONS WHERE UNITY OF INVENTION IS LACKING This application contains the following inventions or groups of inventions which are not so linked as to form a single general inventive concept under PCT Rule 13.1. In order for all inventions to be examined, the appropriate additional examination fees must be paid.

Groups I-XXVII, claim(s) 1-13 and 25-27, drawn to transgenic plants with modified environmental stress tolerance, polynucleotides and vectors for producing said transgenic plants, and methods of making said transgenic plants. Applicant must elect one pair of sequences (one nucleotide sequence and its corresponding amino acid translation) per Group to be examined, *i.e.* SEQ ID NOS: 1 and 2 in Group I, SEQ ID NOS: 3 and 4 in Group II, SEQ ID NOS: 5 and 6 in Group III, etc.

Group XXVIII, claim(s) 15-17, drawn to a method of identifying a factor that is modulated by or interacts with a polypeptide.

Group XXIX, claim(s) 18, drawn to a method of identifying a molecule that modulates activity or expression of a polynucleotide or polypeptide of interest.

Group XXX, claim(s) 19 and 20, drawn to an integrated system, computer, or computer readable medium.

Group XXXI, claim(s) 21-23, drawn to a method of identifying a polynucleotide sequence.

The inventions listed as Groups I-XXXI do not relate to a single general inventive concept under PCT Rule 13.1 because, under PCT Rule 13.2, they lack the same or corresponding special technical features for the following reasons: Groups I-XXVII are drawn to transgenic plants and methods of producing said plants with nucleic acid sequences. The methods of Groups I-XXVII differ from each other in that they are directed to plant transformation methods and transgenic plants with structurally and functionally distinct nucleic acid sequences which encode structurally and functionally different amino acid sequences. In addition, Groups XXVIII, XXIX, and XXXI are different methods from any of Groups I-XXVII in that they have different method steps and different end products, and Group XXX requires a computer system. Thus, there is no single special technical feature which links the inventions of Groups I-XXXI under PCT Rule 13.2.

Continuation of B. FIELDS SEARCHED Item 3: STN (agricola, biosis, biotechno, biotechds, biotechabs, caba, caplus, embase, medline, uspatfull, wpids, pctfull, europatfull, japio) SEARCH TERMS: inventor names, plant transcription factor, stress tolerance; STIC sequence search for SEQ ID NOS: 1 and 2